



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 161268**

**TO: Sumesh Kaushal  
Location: REM-2B85&2C70  
Art Unit: 1633  
Monday, August 08, 2005**

**Case Serial Number: 10/787382**

**From: Alex Waclawiw  
Location: Biotech-Chem Library  
Rem 1A71  
Phone: 272-2534**

**Alexandra.waclawiw@uspto.gov**

### **Search Notes**

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: August 4, 2005, 17:01:52 ; Search time 33.9036 Seconds  
(without alignments)  
295.042 Million cell updates/sec

Title: US-10-787-382-5  
Perfect score: 696  
Sequence: 1 MRRLNLMLALGAAVYSAF.....FLDYLQVFLGVINTWTPES 134

Scoring table: BLOSUM62  
Gapop 10.0 , Gapect 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCBUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1a1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	100.0	134	4	US-09-322-409-81
2	696	100.0	134	4	US-09-451-527-81
3	687	98.7	134	4	US-09-371-615A-2
4	610	87.6	115	4	US-09-322-409-86
5	610	87.6	115	4	US-09-451-527-86
6	430	61.8	134	1	US-08-284-393B-13
7	430	61.8	134	3	US-08-759-628-9
8	430	61.8	134	4	US-09-371-615A-7
9	430	61.8	134	4	US-09-462-941-12
10	430	61.8	134	5	PCT-US95-08950-13
11	430	61.8	134	6	5324640-2
12	430	61.8	134	6	5324640-2
13	376	54.0	133	4	US-09-371-615A-8
14	356	51.1	115	4	US-09-556-818-1
15	351	50.4	121	4	US-09-180-864-2
16	339	48.7	126	4	US-09-556-818-6
17	335	48.1	132	4	US-09-556-818-10
18	332.5	47.8	126	4	US-09-556-818-12
19	332.5	47.8	126	4	US-09-556-818-28
20	331.5	47.6	132	4	US-09-556-818-60
21	330.5	47.5	124	4	US-09-556-818-4
22	330.5	47.5	124	4	US-09-556-818-4
23	329.5	47.3	132	4	US-09-556-818-7
24	328.5	47.2	130	4	US-09-556-818-9
25	328.5	47.2	130	4	US-09-556-818-32
26	324	46.6	147	4	US-09-556-818-42
27	322.5	46.3	130	4	US-09-556-818-14

28	321.5	46.2	124	4	US-09-556-818-5	Sequence 5, Appl
29	321.5	46.2	124	4	US-09-556-818-38	Sequence 38, Appl
30	321	46.1	124	4	US-09-556-818-17	Sequence 17, Appl
31	319.5	45.9	124	4	US-09-556-818-46	Sequence 46, Appl
32	318.5	45.8	130	4	US-09-556-818-56	Sequence 56, Appl
33	317	45.5	113	4	US-09-556-818-12	Sequence 12, Appl
34	317	45.5	128	4	US-09-556-818-21	Sequence 21, Appl
35	315.5	45.3	138	4	US-09-556-818-50	Sequence 50, Appl
36	311	44.7	145	4	US-09-556-818-60	Sequence 60, Appl
37	309.5	44.5	128	4	US-09-556-818-58	Sequence 58, Appl
38	308.5	44.3	122	4	US-09-556-818-54	Sequence 54, Appl
39	301.5	43.3	118	4	US-09-556-818-36	Sequence 36, Appl
40	301.5	43.3	118	4	US-09-556-818-3	Sequence 3, Appl
41	300.5	43.2	141	4	US-09-556-818-11	Sequence 11, Appl
42	299.5	43.0	124	4	US-09-556-818-8	Sequence 8, Appl
43	299.5	43.0	124	4	US-09-556-818-13	Sequence 13, Appl
44	293.5	42.2	124	4	US-09-556-818-15	Sequence 15, Appl
45	291.5	41.9	122	4	US-09-556-818-15	Sequence 18, Appl
46	290.5	41.7	130	4	US-09-556-818-18	Sequence 52, Appl
47	289.5	41.6	116	4	US-09-556-818-52	Sequence 20, Appl
48	289.5	41.6	128	4	US-09-556-818-20	Sequence 48, Appl
49	287.5	41.3	122	4	US-09-556-818-48	Sequence 16, Appl
50	282.5	40.6	139	4	US-09-556-818-16	Sequence 22, Appl
51	282.5	40.6	139	4	US-09-556-818-22	Sequence 14, Appl
52	263.5	37.9	116	4	US-09-556-818-14	Sequence 19, Appl
53	261.5	37.6	122	4	US-09-556-818-19	Sequence 62, Appl
54	75	10.8	19	4	US-09-556-818-62	Sequence 280, App
55	74.5	10.7	407	4	US-09-489-847-280	Sequence 535, Ap
56	74	10.6	333	4	US-09-134-000C-5535	Sequence 33, Appl
57	72.5	10.4	686	4	US-09-914-259-33	Sequence 4, Appl
58	72	10.3	15	5	PCT-US94-06655-4	Sequence 6557, Ap
59	71.5	10.3	521	4	US-09-543-681A-6657	Sequence 20368, A
60	71.5	10.3	593	4	US-09-352-991A-20368	Sequence 5834, Ap
61	71.5	10.3	673	4	US-09-328-352-5834	Sequence 46792, A
62	71.5	10.3	633	4	US-09-270-767-46792	Sequence 7087, Ap
63	70.5	10.1	429	4	US-09-328-352-7087	Sequence 6369, Ap
64	69.5	10.0	312	4	US-09-107-532A-6369	Sequence 2, Appl
65	69.5	10.0	976	3	US-08-560-005-2	Sequence 14, Appl
66	69.5	10.0	976	3	US-09-195-868-14	Sequence 2, Appl
67	69.5	10.0	976	3	US-09-418-540-2	Sequence 8, Appl
68	69.5	10.0	976	3	US-09-969-928-2	Sequence 13016, A
69	69.5	10.0	1187	3	US-08-664-962B-8	Sequence 18473, A
70	69.5	10.0	1187	3	US-09-311-743-8	Sequence 14, Appl
71	69.5	10.0	1187	3	US-09-311-743-8	Sequence 2, Appl
72	69.5	10.0	1189	3	US-09-195-868-15	Sequence 15, Appl
73	68.5	9.8	517	4	US-09-195-868-28	Sequence 28, Appl
74	68	9.8	219	4	US-09-248-796A-14631	Sequence 14631, A
75	68	9.8	257	4	US-09-248-796B-12314	Sequence 21314, A
76	68	9.8	262	4	US-09-248-796A-14638	Sequence 14638, A
77	68	9.8	262	4	US-09-270-767-45972	Sequence 45972, A
78	67.5	9.8	406	4	US-09-902-540-13016	Sequence 13016, A
79	67.5	9.7	224	4	US-09-809-665A-10	Sequence 10, Appl
80	67.5	9.7	344	4	US-09-252-991A-18473	Sequence 18473, A
81	67.5	9.7	968	1	US-08-434-730-14	Sequence 14, Appl
82	67.5	9.7	1185	1	US-08-664-962B-2	Sequence 2, Appl
83	67.5	9.7	1185	3	US-09-311-743-2	Sequence 2, Appl
84	67	9.6	2311	3	US-08-934-386-9	Sequence 9, Appl
85	66.5	9.6	474	4	US-09-710-279-946	Sequence 946, App
86	66.5	9.6	455	3	US-09-134-001C-4294	Sequence 4294, Ap
87	66.5	9.6	604	4	US-09-543-681A-4194	Sequence 4194, Ap
88	66	9.5	465	4	US-09-902-540-10284	Sequence 10284, A
89	66	9.5	465	4	US-09-240-639-8	Sequence 8, Appl
90	66	9.5	465	4	US-09-557-800C-56	Sequence 56, Appl
91	66	9.5	465	4	US-09-370-625A-39	Sequence 39, Appl
92	66	9.5	465	4	US-09-808-510A-8	Sequence 8, Appl
93	66	9.5	465	4	US-09-905-744B-8	Sequence 8, Appl
94	66	9.5	465	4	US-10-107-660-8	Sequence 8, Appl
95	66	9.5	465	4	US-10-107-576-8	Sequence 8, Appl
96	66	9.5	465	4	US-09-905-732B-8	Sequence 8, Appl
97	66	9.5	465	4	US-09-905-743B-8	Sequence 8, Appl
98	66	9.5	394	4	US-09-328-352-6926	Sequence 626, Ap
99	66	9.5	2335	3	US-08-417-089-6	Sequence 6, Appl
100	66	9.5	2335	3	US-08-695-651-6	Sequence 6, Appl

## ALIGNMENTS

## RESULT 1

US-09-322-409-81  
Sequence 81, Application US/09322409  
Patent No. 6471957  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Dreitz, Matthew J.  
APPLICANT: Wondertling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C1  
CURRENT APPLICATION NUMBER: US/09/322,409  
CURRENT FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306  
EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 81  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-09-322-409-81

Query Match 100.0%; Score 696; DB 4; Length 134;

Best Local Similarity 100.0%; Pred. No. 5e-81;

Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLMLNLSLALGAAYSAFAVENPMNRLVAETLTLLSTRTWLIGDGNLMIPTPENKQH 60  
DB 1 MRLMLNLSLALGAAYSAFAVENPMNRLVAETLTLLSTRTWLIGDGNLMIPTPENKQH 60  
QY 61 QLCIKVFGIDITLKNQTAHGAVDKLFONLSLKEHIEROKRCAGERRVTKFLDYIQ 120  
DB 61 QLCIKVFGIDITLKNQTAHGAVDKLFONLSLKEHIEROKRCAGERRVTKFLDYIQ 120  
QY 121 VFISGVINTEWTPES 134  
DB 121 VFISGVINTEWTPES 134

## RESULT 2

US-09-451-527-81  
Sequence 81, Application US/09451527  
Patent No. 6482403  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Dreitz, Matthew J.  
APPLICANT: Wondertling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/09/451,527  
CURRENT FILING DATE: 1999-12-01  
EARLIER APPLICATION NUMBER: 09/322,409  
EARLIER FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306  
EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 81  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-09-451-527-81

Query Match 100.0%; Score 696; DB 4; Length 134;

Best Local Similarity 100.0%; Pred. No. 5e-81;

Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLMLNLSLALGAAYSAFAVENPMNRLVAETLTLLSTRTWLIGDGNLMIPTPENKQH 60  
DB 1 MRLMLNLSLALGAAYSAFAVENPMNRLVAETLTLLSTRTWLIGDGNLMIPTPENKQH 60  
QY 61 QLCIKVFGIDITLKNQTAHGAVDKLFONLSLKEHIEROKRCAGERRVTKFLDYIQ 120  
DB 61 QLCIKVFGIDITLKNQTAHGAVDKLFONLSLKEHIEROKRCAGERRVTKFLDYIQ 120  
QY 121 VFISGVINTEWTPES 134  
DB 121 VFISGVINTEWTPES 134

## RESULT 3

US-09-371-615A-2  
Sequence 2, Application US/09371615A  
Patent No. 6537781  
GENERAL INFORMATION:  
APPLICANT: IDEXX LABORATORIES  
TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING  
FILE REFERENCE: 03604001700US00  
CURRENT APPLICATION NUMBER: US/09/371,615A  
CURRENT FILING DATE: 1999-08-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-09-371-615A-2

Query Match 98.7%; Score 687; DB 4; Length 134;

Best Local Similarity 99.3%; Pred. No. 7.1e-80;

Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRLMLNLSLALGAAYSAFAVENPMNRLVAETLTLLSTRTWLIGDGNLMIPTPENKQH 60  
DB 1 MRLMLNLSLALGAAYSAFAVENPMNRLVAETLTLLSTRTWLIGDGNLMIPTPENKQH 60  
QY 61 QLCIKVFGIDITLKNQTAHGAVDKLFONLSLKEHIEROKRCAGERRVTKFLDYIQ 120  
DB 61 QLCIKVFGIDITLKNQTAHGAVDKLFONLSLKEHIEROKRCAGERRVTKFLDYIQ 120  
QY 121 VFISGVINTEWTPES 134  
DB 121 VFISGVINTEWTPES 134

## RESULT 4

US-09-322-409-86  
Sequence 86, Application US/09322409  
Patent No. 6471957  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Dreitz, Matthew J.  
APPLICANT: Wondertling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C1  
CURRENT APPLICATION NUMBER: US/09/322,409  
CURRENT FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306  
EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 86  
LENGTH: 115  
TYPE: PRT



ORGANISM: Canis familiaris  
US-09-322-409-86

Query Match  
Best Local Similarity 100.0%; Pred. No. 4,1e-70; Length 115;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 FAVENPMNRILVAETLLSTHRTWLIGDGNLMIPTPENKXHQLCIKVFGSIDTLKNQTA 60  
QY 80 HGEAVDKLFQNLISLKEHIEROKKRCGERWRVTKFLDYQVFLGVINTWTPES 134  
DB 61 HGEAVDKLFQNLISLKEHIEROKKRCGERWRVTKFLDYQVFLGVINTWTPES 115

RESULT 5  
US-09-451-527-86

Sequence 86, Application US/09451527  
Patent No. 6482403  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-kee  
APPLICANT: Yang, Shumin  
APPLICANT: Dreitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/09/451,527  
CURRENT FILING DATE: 1999-12-01  
EARLIER APPLICATION NUMBER: 09/322,409  
EARLIER FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306  
EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 86  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-09-451-527-86

Query Match  
Best Local Similarity 100.0%; Pred. No. 4,1e-70; Length 115;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 FAVENPMNRILVAETLLSTHRTWLIGDGNLMIPTPENKXHQLCIKVFGSIDTLKNQTA 60  
QY 80 HGEAVDKLFQNLISLKEHIEROKKRCGERWRVTKFLDYQVFLGVINTWTPES 134  
DB 61 HGEAVDKLFQNLISLKEHIEROKKRCGERWRVTKFLDYQVFLGVINTWTPES 115

RESULT 6  
US-08-284-393B-13

Sequence 13, Application US/08284393B  
Patent No. 5696234  
GENERAL INFORMATION:  
APPLICANT: Zurawski, Sandra M.  
APPLICANT: Zurawski, Gerard  
TITLE OF INVENTION: MUTINS OF MAMMALIAN CYTOKINES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNA Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,393B  
FILING DATE: 01-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0389  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 134 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-284-393B-13

Query Match  
Best Local Similarity 61.8%; Score 430; DB 1; Length 134;  
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

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DB 1 MRWLNLSTLAAAGAAVSAFAVENPMNRILVAETLLSTHRTWLIGDGNLMIPTPENKX 60  
QY 61 QLCIKVFGSIDTLKNQTAHGEAVDKLFQNLISLKEHIEROKKRCGERWRVTKFLDYQ 120  
DB 61 QLCIKVFGSIDTLKNQTAHGEAVDKLFQNLISLKEHIEROKKRCGERWRVTKFLDYQ 120  
QY 121 VFLGVINTWTPES 134  
DB 121 EFLGVNTWTPES 134

RESULT 7  
US-08-759-628-9

Sequence 9, Application US/08759628  
Patent No. 6225446  
GENERAL INFORMATION:  
APPLICANT: Altman, Scott W.  
APPLICANT: Rock, Fernando L.  
APPLICANT: Bazan, J. Fernando  
APPLICANT: Kastelein, Robert A.  
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNA Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/759,628  
FILING DATE: 05-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,574  
FILING DATE: 06-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090

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? REFERENCE/DOCKET NUMBER: DX0552Q
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-852-9196
? TELEFAX: 415-496-1200
? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 134 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? FEATURE:
? NAME/KEY: Peptide
? LOCATION: 20..134
? OTHER INFORMATION: /note="Peptide of Figure 1"
US-08-759-628-9

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Query Match	61.8%	Score	430	DB 3	Length	134	
Best Local Similarity	64.9%	Pred. No.	5.8e-47				
Matches	87	Conservative	17	Mismatches	30	Gaps	0

[illegible]

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QY      121 VFLGVINTEWTPES 134
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Db      121 EFLGVMTIEWIIES 134
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RESULT 8  
US-09-371-615A-7  
: Sequence 7 Application US/09371615A

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1  APPLICANT: IDEXX LABORATORIES
2  TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
3  TITLE OF INVENTION: CANINE INTERLEUKIN 5
4  FILE REFERENCE: 03604001700US/00
5  CURRENT APPLICATION NUMBER: US/09/371,615A
6  CURRENT FILING DATE: 1999-08-10
7  NUMBER OF SEQ ID NOS: 8
8  SOFTWARE: FastSeq for Windows Version 3.0
9  SEQ ID NO 7
10 LENGTH: 134
11 TYPE: PRT
12 ORGANISM: Homo sapiens
13 FEATURE:
14 OTHER INFORMATION: Interleukin 5
15 US-09-371-615A-7

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Query Match      61.8%  Score 430; DB 4; Length 134;
Best Local Similarity 64.9%  Pred No. 5.8e-47;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

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[illegible]

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121  EFGLVMTIEWIES  134

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## RESULT 9

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US-09-462-941-12
? Sequence 12, Application US/09462941
? Patent No. 6608183
? GENERAL INFORMATION:
? APPLICANT: Cox III, George N
? APPLICANT: Bolder Biotechnology, Inc.
? TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
? FILE REFERENCE: 4152-1-PUS
? CURRENT APPLICATION NUMBER: US/09/462,941
? CURRENT FILING DATE: 2000-01-14
? PRIOR APPLICATION NUMBER: 60/052,516
? PRIOR FILING DATE: 1997-07-14
? NUMBER OF SEQ ID NOS: 41
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 12
? LENGTH: 134
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-462-941-12

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Query Match	61.8%	Score	430	DB	4	Length	134
Best Local Similarity	64.9%	Pred. No.	5.8e-47				
Matches	87	Conservative	17	Mismatches	30	Indels	0
						Gaps	0

[illegible]

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QY      121 VFLGVINTEWTPES 134
        ||||:||||
Db      121 EFLGVNTEWIIES 134

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RESULT 10  
PCT-US95-08950-13  
Sequence 13, Application PC/TUS9508950

APPLICANT: Zurawski, Sandra M.  
 APPLICANT: Zurawski, Gerard  
 TITLE OF INVENTION: MOTILINS OF MAMMALIAN CYTOKINES  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: DNAX Research Institute  
 STREET: 901 California Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/08950

1 PRIORITY: 1  
2  
3 PRIOR APPLICATION DATA: 1  
4 APPLICATION NUMBER: US 08/284,392 1  
5 FILING DATE: 01-AUG-1994 1  
6 ATTORNEY/AGENT INFORMATION: 1  
7 NAME: Ching, Edwin P. 1  
8 REGISTRATION NUMBER: 34,090 1  
9 REFERENCE/DOCKET NUMBER: DX0389 1  
0 TELECOMMUNICATION INFORMATION: 1  
1 TELEPHONE: 415-852-9196 1  
2 TELEFAX: 415-496-1200 1  
3 INFORMATION FOR SEQ ID NO: 13: 1  
4 SEQUENCE CHARACTERISTICS: 1

LENGTH: 134 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-08950-13

Query Match 61.8%; Score 430; DB 5; Length 134;  
Best Local Similarity 64.9%; Pred. No. 5.8e-47;  
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSLALGAAYVASAPAVENPMRLVAETLTLLSTRHWLIGDGNLMTPTPENKNH 60  
DB 1 MRMLNLSLALGAAYVAIPTEIPTSALVKETALLSTRHTLLIANETLRIPVPAKHN 60  
QY 61 QLCIKVFGQIDTLKNOTAHGEAVDKLFQNLSTLKEHIEROKKRCAGERRRVTKFLDYIQ 120  
DB 61 QLCIEBIFQIGLTSQTVGGTVERRLPKNLSLTKKYIDQKKKCGERRRVNQFLDYIQ 120  
QY 121 VFLGVNTEWTPES 134  
DB 121 EFLGVNTEWTPES 134

RESULT 11  
5324640-2  
PATENT No. 5324640  
APPLICANT: Honjo, Tasuku/Takatsu, Kiyoshi/Severinson, Eva  
TITLE OF INVENTION: HUMAN B-CELL DIFFERENTIATION FACTOR AND  
PROCESS OF PRODUCING SAID FACTOR  
NUMBER OF SEQUENCES: 2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-07/99,467  
FILING DATE: 21-SEP-1987  
SEQ ID NO: 2  
LENGTH: 134

Query Match 61.8%; Score 430; DB 6; Length 134;  
Best Local Similarity 64.9%; Pred. No. 5.8e-47;  
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSLALGAAYVASAPAVENPMRLVAETLTLLSTRHWLIGDGNLMTPTPENKNH 60  
DB 1 MRMLNLSLALGAAYVAIPTEIPTSALVKETALLSTRHTLLIANETLRIPVPAKHN 60  
QY 61 QLCIKVFGQIDTLKNOTAHGEAVDKLFQNLSTLKEHIEROKKRCAGERRRVTKFLDYIQ 120  
DB 61 QLCIEBIFQIGLTSQTVGGTVERRLPKNLSLTKKYIDQKKKCGERRRVNQFLDYIQ 120  
QY 121 VFLGVNTEWTPES 134  
DB 121 EFLGVNTEWTPES 134

RESULT 12  
5324640-2  
PATENT No. 5324640  
APPLICANT: Honjo, Tasuku/Takatsu, Kiyoshi/Severinson, Eva  
TITLE OF INVENTION: HUMAN B-CELL DIFFERENTIATION FACTOR AND  
PROCESS OF PRODUCING SAID FACTOR  
NUMBER OF SEQUENCES: 2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-07/99,467  
FILING DATE: 21-SEP-1987  
SEQ ID NO: 2  
LENGTH: 134

Query Match 61.8%; Score 430; DB 6; Length 134;  
Best Local Similarity 64.9%; Pred. No. 5.8e-47;  
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSLALGAAYVASAPAVENPMRLVAETLTLLSTRHWLIGDGNLMTPTPENKNH 60  
DB 1 MRMLNLSLALGAAYVAIPTEIPTSALVKETALLSTRHTLLIANETLRIPVPAKHN 60  
QY 61 QLCIKVFGQIDTLKNOTAHGEAVDKLFQNLSTLKEHIEROKKRCAGERRRVTKFLDYIQ 120  
DB 61 QLCIEBIFQIGLTSQTVGGTVERRLPKNLSLTKKYIDQKKKCGERRRVNQFLDYIQ 120  
QY 121 VFLGVNTEWTPES 134  
DB 121 EFLGVNTEWTPES 134

RESULT 13  
US-09-371-615A-8  
Sequence 8, Application US/09371615A  
Patent No. 6537781  
GENERAL INFORMATION:  
APPLICANT: IDEXX LABORATORIES  
TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING  
TITLE OF INVENTION: CANINE INTERLEUKIN 5  
FILE REFERENCE: 03604001700US00  
CURRENT APPLICATION NUMBER: US/09/371,615A  
CURRENT FILING DATE: 1999-08-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 8  
LENGTH: 133  
TYPE: PRT  
ORGANISM: Mus musculus  
FEATURE:  
OTHER INFORMATION: Interleukin 5  
US-09-371-615A-8

Query Match 54.0%; Score 376; DB 4; Length 133;  
Best Local Similarity 56.8%; Pred. No. 4.7e-40;  
Matches 75; Conservative 21; Mismatches 34; Indels 2; Gaps 1;

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DB 3 RMLNLSLALGAAYVAIPTEIPTSALVKETALLSTRHTLLIANETLRIPVPAKHN 60  
QY 62 LCIKEVFGQIDTLKNOTAHGEAVDKLFQNLSTLKEHIEROKKRCAGERRRVTKFLDYIQ 121  
DB 62 LCIKEVFGQIDTLKNOTAHGEAVDKLFQNLSTLKEHIEROKKRCAGERRRVTKFLDYIQ 120  
QY 122 VFLGVNTEWTPES 133  
DB 121 EFLGVNTEWTPES 132

RESULT 14  
US-09-556-818-1  
Sequence 1, Application US/09556818  
Patent No. 6746669  
GENERAL INFORMATION:  
APPLICANT: Kiyner, Steen  
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity  
FILE REFERENCE: 0459-0428P  
CURRENT APPLICATION NUMBER: US/09/556,818  
CURRENT FILING DATE: 2000-04-21  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DISULFID  
LOCATION: (44)  
OTHER INFORMATION: Interchain disulphide bond to Cys-86 in SEQ ID  
NAME/KEY: DISULFID

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: LOCATION: (86)
: OTHER INFORMATION: Interchain disulphide bond to Cys-44 in SEQ ID
: OTHER INFORMATION: NO:1
US-09-556-818-1

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Query Match	51.1%	Score	356	DB 4	length	115	
Best Local Similarity	62.5%	Pred. No.	1.4e-37				
Matches	70	Conservative	16	Mismatches	26	Gaps	0

Qy 23 ENPMRLVAETLLSTHRTWLGDNMIPTPENKHOCIKVYQGISDILKNQAHGE 82  
| : | | | | | | | : | | | | | : | | | | | : | : | |  
Do 4 EIPISALVKETALLSTHRTLLIANETURIPIVPVPHKNHOCSTEBIFQGISGTLSQTVQGG 63

```

QY      83 AVDDKLFQNTSLIKEHIERQKRCAGERNRTKFLDYQVFLGVINTEMTPE 134
      |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      64 TVERLEKNLSLIKCYIDGQKKCGEERRRVAQFLDYQVFLGVNTEMTPE 115

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RESULT 15  
MS-09-190

US-09-180-864-2  
; Sequence 2, Application US/09180864

**! GENERAL INFORMATION:**

```

; APPLICANT: Lopez, Angel
; APPLICANT: Vadas, Matthew

```

APPLICANT: Bastiras, Stan

**TITLE OF INVENTION: AN INTERLEUKIN-5 ANTAGONIST**

**CURRENT APPLICATION NUMBER: US/09/180,864**

PRIOR APPLICATION NUMBER: 08/591,438

; NUMBER OF SEQ ID NOS: 8

SEQ ID NO 2	SEQ ID NO 1
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TYPE: PRT

US-09-180-864-2

Query Match	50.4%
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Matched 69:

23 Oy

10 Db

83 AVDKL.FONT.SL.TK

70 T  
nh

Search completed: August 4, 2005, 17:13:06  
Job time : 35.9036 secs

[illegible]

Search completed: August 4, 2005, 17:13:06  
Job time : 35.9036 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using fframe\_p2n model

Run on: August 6, 2005, 19:38:05 ; Search time 2459.9 Seconds

(without alignments)  
2639.542 Million cell updates/sec

Title: US-10-787-382-5

Perfect score: 696

Sequence: 1 MRMLNLSLALGAAVYSAF.....FLDYLGVLGIVNTEWTPES 134

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Genemb1:\*  
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2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_on:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	100.0	402	6	BD211560 Canine an
2	696	100.0	402	6	BD211561 Canine an
3	696	100.0	402	6	AR241538 Sequence
4	696	100.0	402	6	AR241539 Sequence

5	696	100.0	402	6	AR254494 Sequence
6	696	100.0	402	6	AR254495 Sequence
7	696	100.0	610	4	AR31919 Canis fam
8	696	100.0	610	6	BD211558 Canine an
9	696	100.0	610	6	BD211559 Canine an
10	696	100.0	610	6	AR241536 Sequence
11	696	100.0	610	6	AR241537 Sequence
12	696	100.0	610	6	AR254492 Sequence
13	696	100.0	610	6	AR254493 Sequence
14	687	98.7	405	6	AR300436 Sequence
15	687	98.7	405	6	AX083939 Sequence
16	610	87.6	345	6	BD211562 Canine an
17	610	87.6	345	6	BD211563 Canine an
18	610	87.6	345	6	AR241540 Sequence
19	610	87.6	345	6	AR241541 Sequence
20	610	87.6	345	6	AR254496 Sequence
21	610	87.6	345	6	AR254497 Sequence
22	591	84.9	838	4	AF025436 Felis cat
23	586	84.2	405	4	AF068770 Felis cat
24	578	83.0	405	4	SSC010088 Sus scrofa
25	578	83.0	529	4	SSC133452 Sus scrofa
26	571	82.0	356	4	AF091133 Canis fam
27	567	81.5	405	4	ECU91947 Equus caball
28	551	79.2	405	4	BTINTLEB05 B. taurus mr
29	541	77.7	520	4	OAUS35038 Ovis aries
30	468	67.2	354	4	AF051372 Felis cat
31	448	64.4	405	9	AF294756 Canis fam
32	444	63.8	405	6	AX083948 Canis fam
33	430	61.8	421	12	SYN1LSA M33949 Synthetic h
34	430	61.8	459	9	BC066282 Homo sapi
35	430	61.8	816	6	C0721603 Sequence
36	430	61.8	816	6	B01639 cDNA encodi
37	430	61.8	816	6	E13591 cDNA encodi
38	430	61.8	816	6	HS1LSR X04688 Human mRNA
39	430	61.8	858	6	AX766521 Sequence
40	430	61.8	858	6	AX766523 Sequence
41	430	61.8	4946	1	PV1RES Y07702 Plasmid pV
42	429	61.6	405	9	CEY1NSA L36033 Carcovebus
43	426	61.2	405	9	MMU19848 Mus mus
44	424	60.9	816	6	AR380691 Sequence
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#### ALIGNMENTS

RESULT 1	BD211560	402 bp	DNA	linear	PAT 17-JUN-2003
LOCUS	BD211560				
DEFINITION	Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same.				
ACCESSION	BD211560	1	GI:33021330		
VERSION	BD211560.1				
KEYWORDS	JP 2002516104-A/66.				
SOURCE	Canis familiaris (dog)				
ORGANISM	Canis familiaris				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butcheria; Carnivora; Fissipedia; Canidae; Canis.				
AUTHORS	Sim,G., Yang,S., Dretz,M.J. and Wonderling,R.S.				
TITLE	Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same				
JOURNAL	Patent: JP 2002516104-A 66 04-JUN-2002;				
COMMENT	HEKSA CORP				
OS	Canis familiaris (dog)				
PN	JP 2002516104-A/66				
PD	04-JUN-2002				
PF	28-MAY-1999 JP 2000551002				
PI	29-MAY-1998 US 60/087306				
PC	CEKKEB SIM,SHUMIN YANG,MATTHEW J DRETZ,RAMANI S WONDERLING PC				
PC	CI2N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/355,				
PC	A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,				
PC	C07K14/54,				

PC C07K14/56, C07K14/705, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC  
G01N33/15,  
PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine  
and feline immunoregulatory proteins, nucleic acid CC  
molecules and  
CC method of using the same  
FT Key Location/Qualifiers  
FT source 1..402 /organism='Canis familiaris (dog)'.  
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ORIGIN

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Pred. No.:	1,27e-75	Length:	402
Score:	696.00	Matches:	134
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-787-382-5 (1-134) x BD211560 (1-402)

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DB 1 ATGAGAAATGCTTCTGGAATTTGAGTTTCTACCTTTGGGCTGCTATGTTTCTGCTTT 60  
QY 21 AlaValGluAnPProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40  
DB 61 GCTGTAGAAAATCCCATGAAATAGACTGTGGCAGAGACCTTGACATGCTCTCCACTCAT 120  
QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAnLeuYsaAnHis 60  
DB 121 CGAAGTGGCTGATAGGCGATGAGAACCTGATGATTCCTACTCTGAAAATTAATAATCAC 180  
QY 61 GluLeuCySIIeLysGluValPheGlnGlyIleAspThrLeuYsaAnGlnThrAlaHis 80  
DB 181 CAACGTGCATTAAAGAAAGTTTTCAGGGTATACACATTTGAAGAACCAAACTGCCAC 240  
QY 81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100  
DB 241 GGGAGGCTGTGATTAACATATTCCTCAAACTGTCTTAATTAAGAACACATAGAGCGC 300  
QY 101 GlnLysLysArgCySAlaGlyGluArgTrpArgValThrLysPheLeuAspTrpLeuGln 120  
DB 301 CAAAAAAGAGTGTGAGGAGAAAGATGAGAGTGAACAAAGTTCTTAACTACTGCA 360  
QY 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
DB 361 GTATTTCTTGTGTATTAACACCGAGTGAACCGGAAGT 402

RESULT 2  
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LOCUS Canine and feline immunoregulatory proteins, nucleic acid molecules  
DEFINITION and method of using the same.  
ACCESSION BD211561  
VERSION BD211561.1 GI:33021331  
KEYWORDS JP 2002516104-A/67.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Plissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 402)  
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules  
and method of using the same  
JOURNAL Patent: JP 2002516104-A 67 04-JUN-2002;  
HESKA CORP  
COMMENT OS Canis familiaris (dog)

PN JP 2002516104-A/67  
PD 04-JUN-2002  
PR 28-MAY-1999 JP 2000551002  
PR 29-MAY-1998 US 60/087306  
PI GEKKEB SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANT S WONDERLING, PC  
C12N15/00, A61K31/7088, A61K38/00, A61K38/21, A61K39/00, A61K39/395,  
PC A61K39/395,  
PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,  
PC C07K14/54,  
PC C07K14/56, C07K14/705, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC  
G01N33/15  
PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine  
and feline immunoregulatory proteins, nucleic acid CC  
molecules and  
CC method of using the same  
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FT source 1..402 /organism='Canis familiaris (dog)'.  
Location/Qualifiers  
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ORIGIN

Alignment Scores:

Pred. No.:	1,27e-75	Length:	402
Score:	696.00	Matches:	134
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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DB:	6	Gaps:	0

US-10-787-382-5 (1-134) x BD211561 (1-402)

QY 1 MetArgMetLeuLeuAnLeuSerLeuLeuAlaLeuGlyAlaAlaIYrValSerAlaPhe 20  
DB 402 ATGAGAAATGCTTCTGGAATTTGAGTTTCTACCTTTGGGCTGCTATGTTTCTGCTTT 363  
QY 21 AlaValGluAnPProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40  
DB 342 GCTGTAGAAAATCCCATGAAATAGACTGTGGCAGAGACCTTGACATGCTCTCCACTCAT 283  
QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAnLeuYsaAnHis 60  
DB 282 CGAAGTGGCTGATAGGCGATGAGAACCTGATGATTCCTACTCTGAAAATTAATAATCAC 223  
QY 61 GluLeuCySIIeLysGluValPheGlnGlyIleAspThrLeuYsaAnGlnThrAlaHis 80  
DB 222 CAACGTGCATTAAAGAAAGTTTTCAGGGTATACACATTTGAAGAACCAAACTGCCAC 163  
QY 81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100  
DB 162 GGGAGGCTGTGATTAACATATTCCTCAAACTGTCTTAATTAAGAACACATAGAGCGC 103  
QY 101 GlnLysLysArgCySAlaGlyGluArgTrpArgValThrLysPheLeuAspTrpLeuGln 120  
DB 102 CAAAAAAGAGTGTGAGGAGAAAGATGAGAGTGAACAAAGTTCTTAACTACTGCA 43  
QY 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
DB 42 GTATTTCTTGTGTATTAACACCGAGTGAACCGGAAGT 1

RESULT 3  
AR241538  
LOCUS 402 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 83 from patent US 6471957.  
ACCESSION AR241538  
VERSION AR241538.1 GI:27287247  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
COMMENT Unclassified.

REFERENCE 1 (bases 1 to 402)  
 AUTHORS Sim.G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
 TITLE Canine IL-4 immunoregulatory proteins and uses thereof  
 JOURNAL Patent: US 6471957-A 83 29-OCT-2002;  
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## ORIGIN

Alignment Scores:  
 Pred. No.: 1,27e-75 Length: 402  
 Score: 696.00 Matches: 134  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
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US-10-787-382-5 (1-134) x AR241538 (1-402)

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 Db 1 ATGAGAAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGCGGCTGCTATGTTCTGCCCTT 60  
 Qy 21 AlaValGluAenPrometAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
 Db 61 GCTGTAGAAATCCCATTAATAGACTGTGGGAGAGACCTTGACCTGCTCTCCACTCAT 120  
 Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60  
 Db 121 CGAAGTGGCTGATAGGCGATGGGAACTGATGATCTCTACTCTCGAAATTAATAATCAC 180  
 Qy 61 GlnLeuCySilelyGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80  
 Db 181 CAATGTCATTAAGAAGATTTCAGGGTATAGACATTTGAAGAACCAACTGCCAC 240  
 Qy 81 GlyGluAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIlelyGluHisIleGluArg 100  
 Db 241 GGGAGGCTGTGATTAACCTATTCCTTAATTAATTAATTAATTAATTAATTAATTAATTA 300  
 Qy 101 GlnLysLysArgCySAlaGlyGluArgValThrLysPheLeuAspTyrLeuGln 120  
 Db 301 CAAAAAAGAGTGTGCGAGAGAAAGATGAGAGATGAGAAAGTCTCTAGACTCTGCA 360  
 Qy 121 ValPheLeuGlyValIleAsnThrGluThrProGluSer 134  
 Db 361 GTATTTCTTGCTGTATTAACACCGATGACACCGGAAAGT 402

## RESULT 4

AR241538/c  
 LOCUS AR241539 84 from patent US 6471957. 402 bp DNA linear PAT 20-DEC-2002  
 DEFINITION AR241539  
 ACCESSION AR241539  
 VERSION AR241539.1 GI:27287248  
 KEYWORDS

## SOURCE

ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 402)  
 AUTHORS Sim.G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
 TITLE Canine IL-4 immunoregulatory proteins and uses thereof  
 JOURNAL Patent: US 6471957-A 84 29-OCT-2002;  
 FEATURES Location/Qualifiers  
 source 1..402  
 /organism="unknown"  
 /mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,27e-75 Length: 402  
 Score: 696.00 Matches: 134  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0  
 US-10-787-382-5 (1-134) x AR241539 (1-402)

Qy 1 MetArgMetLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaTyValSerAlaPhe 20  
 Db 402 ATGAGAAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGCGGCTGCTATGTTCTGCCCTT 343  
 Qy 21 AlaValGluAenPrometAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
 Db 342 GCTGTAGAAATCCCATTAATAGACTGTGGGAGAGACCTTGACCTGCTCTCCACTCAT 283  
 Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60  
 Db 282 CGAAGTGGCTGATAGGCGATGGGAACTGATGATCTCTACTCTCGAAATTAATAATCAC 223  
 Qy 61 GlnLeuCySilelyGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80  
 Db 222 CAATGTCATTAAGAAGATTTCAGGGTATAGACATTTGAAGAACCAACTGCCAC 163  
 Qy 81 GlyGluAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIlelyGluHisIleGluArg 100  
 Db 162 GGGAGGCTGTGATTAACCTATTCCTTAATTAATTAATTAATTAATTAATTAATTAATTA 103  
 Qy 101 GlnLysLysArgCySAlaGlyGluArgValThrLysPheLeuAspTyrLeuGln 120  
 Db 102 CAAAAAAGAGTGTGCGAGAGAAAGATGAGAGATGAGAAAGTCTCTAGACTCTGCA 43  
 Qy 121 ValPheLeuGlyValIleAsnThrGluThrProGluSer 134  
 Db 42 GTATTTCTTGCTGTATTAACACCGATGACACCGGAAAGT 1

## RESULT 5

AR254494  
 LOCUS AR254494 83 from patent US 6482403. 402 bp DNA linear PAT 20-DEC-2002  
 DEFINITION AR254494  
 ACCESSION AR254494  
 VERSION AR254494.1 GI:27303382  
 KEYWORDS

## SOURCE

ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 402)  
 AUTHORS Sim.G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
 TITLE Canine IL-13 immunoregulatory proteins and uses thereof  
 JOURNAL Patent: US 6482403-A 83 19-NOV-2002;  
 FEATURES Location/Qualifiers  
 source 1..402  
 /organism="unknown"  
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## ORIGIN

Alignment Scores:  
 Pred. No.: 1,27e-75 Length: 402  
 Score: 696.00 Matches: 134  
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 Best Local Similarity: 100.00% Mismatches: 0  
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US-10-787-382-5 (1-134) x AR254494 (1-402)

Qy 1 MetArgMetLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaTyValSerAlaPhe 20  
 Db 1 ATGAGAAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGCGGCTGCTATGTTCTGCCCTT 60  
 Qy 21 AlaValGluAenPrometAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
 Db 61 GCTGTAGAAATCCCATTAATAGACTGTGGGAGAGACCTTGACCTGCTCTCCACTCAT 120  
 Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60

Db 121 CGAAGTGGCTGATAGGCGATGGAGACCTGATGATCTCTGCTGAAAAATTAATAC 180  
Qy 61 GlnleuCySilelysglValPheGlnGlylleaPheThleuLySaenGlnThraLHis 80  
Db 181 CAACTGGCATTAAGAAAGTTTTCAGGGTATTAACATTAAGAAACCAACTGCCAC 240  
Qy 81 GlnGlnAlaValaAplysLeuPheGlnaSenSerleuilelysglunHsileGluArg 100  
Db 241 GGGGAGGCTGGATTAAGAACTTTCACAAACTTGTCTTAATAAAGAAACATAGAGCGC 300  
Qy 101 GlnleuLySaenCySaAlaGlyGlnArgAlaThryLyPheLeuApyThleuGln 120  
Db 301 CAAAAAAGAGTGTGAGGAGAAAGATGAGAGTGAACAAAGTTCCTAGACTCTGCAA 360  
Qy 121 ValPheleuGlyValilleaenThGluThrThrProGluSer 134  
Db 361 GTATTCTTGCTGATTAACACCGAGTGGACCGGAAAGT 402  
RESULT 6  
AR254495/c 402 bp DNA linear PAT 20-DEC-2002  
LOCUS AR254495 Sequence 84 from patent US 6482403.  
DEFINITION AR254495  
ACCESSION AR254495  
VERSION AR254495.1 GI:27303383  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 402)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-13 Immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6482403-A 84 19-NOV-2002;  
FEATURES  
source 1. 402  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
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Pred. No.: 1,27e-75 Length: 402  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 6  
US-10-787-382-5 (1-134) x AR254495 (1-402)  
Qy 1 MetArgPheLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaTyValSerAlaPhe 20  
Db 402 ATGAGAAATGCTTCTGAATTTGAGTTTGCTAGCTCTGGGCTGCTATGTTTCTGCCCTT 343  
Qy 21 AlaValGlnaenPrometAenArgLeuValAlaGlnThryLeuThryLeuSerThHis 40  
Db 342 GCTATGAAATCCCATGATATAGACTGCTGCGAAGACCTTGACACTGCTCTCCACTCAT 283  
Qy 41 ArgThrTrpLeuileGlyAaPglYasnLeuMetilleProThrProGluAenLySaenHis 60  
Db 282 CGAAGTGGCTGATAGGCGATGGAACCTGATGATCTCTGCTGAAAAAATTAATCAC 223  
Qy 61 GlnleuCySilelysglValPheGlnGlylleaPheThleuLySaenGlnThraLHis 80  
Db 222 CAACTGGCATTAAGAAAGTTTTCAGGGTATTAACATTAAGAAACCAACTGCCAC 163  
Qy 81 GlnGlnAlaValaAplysLeuPheGlnaSenSerleuilelysglunHsileGluArg 100  
Db 162 GGGGAGGCTGGATTAAGAACTTTCACAAACTTGTCTTAATAAAGAAACATAGAGCGC 103  
Qy 101 GlnleuLySaenCySaAlaGlyGlnArgAlaThryLyPheLeuApyThleuGln 120  
Db 102 CAAAAAAGAGTGTGAGGAGAAAGATGAGAGTGAACAAAGTTCCTAGACTCTGCAA 43  
Qy 121 ValPheleuGlyValilleaenThGluThrThrProGluSer 134

Db 42 GTATTCTTGCTGATTAACACCGAGTGGACCGGAAAGT 1  
RESULT 7  
AF331919 610 bp mRNA linear MAM 04-OCT-2001  
LOCUS AF331919  
DEFINITION Canis familiaris Interleukin-5 mRNA, complete cde.  
ACCESSION AF331919  
VERSION AF331919.1 GI:15919180  
KEYWORDS  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 610)  
AUTHORS Yang,S., Seiling,K.S., Weber,B. and McCall,C.  
TITLE Canine interleukin-5: molecular characterization of the gene and expression of biologically active recombinant protein  
JOURNAL J. Interferon Cytokine Res. 21 (6), 361-367 (2001)  
MEDLINE 21334408  
PUBMED 1140633  
REFERENCE 2 (bases 1 to 610)  
AUTHORS Yang,S.  
TITLE Direct Submission  
JOURNAL Submitted (22-DEC-2000) Immunology, Heek Corporation, 1613 Prospect Parkway, Ft Collins, CO 80525, USA  
FEATURES  
source 1. 610  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
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29.. 433  
/note="IL-5"  
/codon\_start=1  
/product="interleukin-5"  
/protein\_id="AAU10715.1"  
/db\_xref="GI:15919181"  
/translation="MRMLNTSLIALGAAYSAFAVENPNRRLVARTLTLSHRTWL  
IGGNLMIPPEKNHOLCIKEVFGIDTKNGNTAAGEAVDKLFQNLISLKEHIEROK  
KRAGGRMRYTRKLDVLYQVFLGVINTEWTPES"  
433.. 610  
ORIGIN  
3' UTR  
Alignment Scores:  
Pred. No.: 2,13e-75 Length: 610  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 4  
US-10-787-382-5 (1-134) x AF331919 (1-610)  
Qy 1 MetArgPheLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaTyValSerAlaPhe 20  
Db 29 ATGAGAAATGCTTCTGAATTTGAGTTTGCTAGCTCTGGGCTGCTATGTTTCTGCCCTT 88  
Qy 21 AlaValGlnaenPrometAenArgLeuValAlaGlnThryLeuThryLeuSerThHis 40  
Db 89 GCTGTAATAATCCCATGATATAGACTGCTGCGAAGACCTTGACACTGCTCTCCACTCAT 148  
Qy 41 ArgThrTrpLeuileGlyAaPglYasnLeuMetilleProThrProGluAenLySaenHis 60  
Db 149 CGAAGTGGCTGATAGGCGATGGAACCTGATGATCTCTGCTGAAAAAATTAATCAC 208  
Qy 61 GlnleuCySilelysglValPheGlnGlylleaPheThleuLySaenGlnThraLHis 80  
Db 209 CAACTGGCATTAAGAAAGTTTTCAGGGTATTAACATTAAGAAACCAACTGCCAC 268  
Qy 81 GlnGlnAlaValaAplysLeuPheGlnaSenSerleuilelysglunHsileGluArg 100  
Db 269 GGGGAGGCTGGATTAAGAACTTTCACAAACTTGTCTTAATAAAGAAACATAGAGCGC 328



Qy 101 GlnlyslsYsargCyAlaGlyGluArgTrpArgValThrlyspheLeuaspTylleuGln 120  
Db 329 CAAAAAAGAGGTGCGAGGAAAGATGAGAGCAAAAGTTCTTACTACTGCA 388

Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
Db 389 GTATTCTTGCTGTATTAACACCGAGTGCACCGGAAAGT 430

RESULT 8  
BD211558 610 bp DNA linear PAT 17-JUN-2003  
LOCUS Canine and feline immunoregulatory proteins, nucleic acid molecules  
DEFINITION BD211558.1 GI:33021328  
ACCESSION BD211558.1 GI:33021328  
VERSION JP 2002516104-A/64.  
KEYWORDS Canis familiaris (dog)  
SOURCE Canis familiaris  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 610)  
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules  
and method of using the same  
JOURNAL Patent: JP 2002516104-A 64 04-JUN-2002;  
HESKA CORP  
OS Canis familiaris (dog)  
PN JP 2002516104-A/64  
PD 04-JUN-2002  
PF 28-MAY-1999 JP 2000551002  
PR 29-MAY-1998 US 60/087306  
PI GEKKEB SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC  
C12N15/09,A61K31/7088,A61K38/00,A61K39/21,A61K39/00,A61K39/395,  
PC A61K39/395,  
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,  
PC C07K14/54,  
PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC  
G01N33/15,  
PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine  
and feline immunoregulatory proteins, nucleic acid CC  
molecules and  
CC method of using the same  
FH Key Location/Qualifiers  
FT CDS (29)..(430).  
Location/Qualifiers  
1..610  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9615"

ORIGIN  
Alignment Scores: 2.13e-75 Length: 610  
Pred. No.: 696.00 Matches: 134  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 6

US-10-787-382-5 (1-134) x BD211558 (1-610)

Qy 1 MetArgMetLeuAanLeuSerLeuAlaLeuGlyAlaIaIaTyValSerAlaPhe 20  
Db 29 ATGGAAGCTTCTGGAATTGAGTTTGTCTTCTTGGGCTGCTTATGTTCTGCTTT 88

Qy 21 AlaValGluAanProMetAsnArgLeuValAlaGluTrpLeuTrpLeuSerThrHis 40  
Db 89 GCTGTGAAGAAATCCCATGATGAGTGTGGAGGACCTTGACACTCTCTCCACTCAT 148

Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAanLysAsnHis 60  
Db 149 CGAAGTGGCTGATAGCGGATGGGAACCTGATGATCTCTACTCCGAAATTAATAATCAC 208

Qy 61 GlnleuCyIleIleYsGluValPheGlnGlyIleAspThrleuLysaenGlnThrAlaHis 80  
Db 209 CAATGTCGATTAAGAAAGTTTTCAGGGTATTAACACATTGAAAGAACCAATGCCAC 268

Qy 81 GlyIleuAlaValaAspLysLeuPheGlnAsnLeuSerleuIleYsGluHisIleGluArg 100  
Db 269 GCGAGGCTGTGATTAACATTTCCAAACCTTGCTTTATTAATAAGAACATGAGGCG 328

Qy 101 GlnlyslsYsargCyAlaGlyGluArgTrpArgValThrlyspheLeuaspTylleuGln 120  
Db 329 CAAAAAAGAGGTGCGAGGAAAGATGAGAGCAAAAGTTCTTACTACTGCA 388

Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
Db 389 GTATTCTTGCTGTATTAACACCGAGTGCACCGGAAAGT 430

RESULT 9  
BD211559/c 610 bp DNA linear PAT 17-JUN-2003  
LOCUS Canine and feline immunoregulatory proteins, nucleic acid molecules  
DEFINITION BD211559  
ACCESSION BD211559.1 GI:33021329  
VERSION JP 2002516104-A/65.  
KEYWORDS Canis familiaris (dog)  
SOURCE Canis familiaris  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 610)  
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules  
and method of using the same  
JOURNAL Patent: JP 2002516104-A 65 04-JUN-2002;  
HESKA CORP  
OS Canis familiaris (dog)  
PN JP 2002516104-A/65  
PD 04-JUN-2002  
PF 28-MAY-1999 JP 2000551002  
PR 29-MAY-1998 US 60/087306  
PI GEKKEB SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC  
C12N15/09,A61K31/7088,A61K38/00,A61K39/21,A61K39/00,A61K39/395,  
PC A61K39/395,  
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,  
PC C07K14/54,  
PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC  
G01N33/15,  
PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine  
and feline immunoregulatory proteins, nucleic acid CC  
molecules and  
CC method of using the same  
FH Key Location/Qualifiers  
FT CDS (29)..(430).  
Location/Qualifiers  
1..610  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9615"

ORIGIN  
Alignment Scores: 2.13e-75 Length: 610  
Pred. No.: 696.00 Matches: 134  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 6

US-10-787-382-5 (1-134) x BD211559 (1-610)

Qy 1 MetArgMetLeuAanLeuSerLeuAlaLeuGlyAlaIaIaTyValSerAlaPhe 20

Db 582 ATGAGAAATGCTTGAATTTGAGTTTGTAGCTTGTGGGCTGCTATGTTTTCGCTTT 523  
Qy 21 ALaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40  
Db 522 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 463  
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleAsnHis 60  
Db 462 CGAACTTGCTGATAGGCGATGGGAACTGATGATTCCTACTCTCTGAAAAATTAATATCAC 403  
Qy 61 GluLeuCyrtIleLeuGluValPheGlnGlyIleAspThrLeuLeuAsnGlnThrAlaHis 80  
Db 402 CAACCTGGACATTAAGAAGATTTTCAGAGTATTAACAACATTGAAGAACCAAACTGCCAC 343  
Qy 81 GlyValAlaValAlaAspLeuPheGlnAsnLeuSerLeuIleLeuGluHisIleGluArg 100  
Db 342 GGGAGGCTGTGATTAACATTTCTCAAACTGTCTTTATTAAGAACAATAGAGCGC 283  
Qy 101 GluLeuLeuAspGlyAlaGlyGluArgTyrArgValThrIlePheLeuAspTyrLeuGln 120  
Db 282 CAATAAAGAGTGTGACAGAGAAAGATGAGAGTGAACAAGTTCTTAGACTACTGCA 223  
Qy 121 ValPheLeuGlyValIleAsnThrGluThrProGluSer 134  
Db 222 GTATTCTTGCTGTATTAACACCGAGTGAACCCGAAAGT 181  
RESULT 10  
LOCUS AR241536 610 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 80 from patent US 6471957.  
ACCESSION AR241536  
VERSION AR241536.1 GI:27287245  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 610)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITL Cantine IL-4 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6471957-A 80 29-OCT-2002;  
FEATURES  
source location/Qualifiers  
1..610  
/organism="unknown"  
/mol\_type="genomic DNA"  
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Alignment Scores: 2.13e-75 Length: 610  
Pred. No.: 696.00 Matches: 134  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
US-10-787-382-5 (1-134) x AR241536 (1-610)  
Qy 1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyValAlaTyrValSerAlaPhe 20  
Db 29 ATGAGAAATGCTTGAATTTGAGTTTGTAGCTTGTGGGCTGCTATGTTTTCGCTTT 88  
Qy 21 ALaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40  
Db 89 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148  
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleAsnHis 60  
Db 149 CGAACTTGCTGATAGGCGATGGGAACTGATGATTCCTACTCTCTGAAAAATTAATATCAC 208  
Qy 61 GluLeuCyrtIleLeuGluValPheGlnGlyIleAspThrLeuLeuAsnGlnThrAlaHis 80  
Db 209 CAACCTGGACATTAAGAAGATTTTCAGAGTATTAACAACATTGAAGAACCAAACTGCCAC 268  
Qy 81 GlyValAlaValAlaAspLeuPheGlnAsnLeuSerLeuIleLeuGluHisIleGluArg 100

Db 269 GGGAGGCTGTGATTAACATTAATCCAAACTGTCTTTATTAAGAACAACATAGAGCGC 328  
Qy 101 GluLeuLeuAspGlyAlaGlyGluArgTyrArgValThrIlePheLeuAspTyrLeuGln 120  
Db 329 CAATAAAGAGTGTGACAGAGAAAGATGAGAGTGAACAAGTTCTTAGACTACTGCA 388  
Qy 121 ValPheLeuGlyValIleAsnThrGluThrProGluSer 134  
Db 389 GTATTCTTGCTGTATTAACACCGAGTGAACCCGAAAGT 430  
RESULT 11  
LOCUS AR241537 610 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 82 from patent US 6471957.  
ACCESSION AR241537  
VERSION AR241537.1 GI:27287246  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 610)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITL Cantine IL-4 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6471957-A 82 29-OCT-2002;  
FEATURES  
source location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"  
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Alignment Scores: 2.13e-75 Length: 610  
Pred. No.: 696.00 Matches: 134  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
US-10-787-382-5 (1-134) x AR241537 (1-610)  
Qy 1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyValAlaTyrValSerAlaPhe 20  
Db 582 ATGAGAAATGCTTGAATTTGAGTTTGTAGCTTGTGGGCTGCTATGTTTTCGCTTT 523  
Qy 21 ALaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40  
Db 522 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 463  
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleAsnHis 60  
Db 462 CGAACTTGCTGATAGGCGATGGGAACTGATGATTCCTACTCTCTGAAAAATTAATATCAC 403  
Qy 61 GluLeuCyrtIleLeuGluValPheGlnGlyIleAspThrLeuLeuAsnGlnThrAlaHis 80  
Db 402 CAACCTGGACATTAAGAAGATTTTCAGAGTATTAACAACATTGAAGAACCAAACTGCCAC 343  
Qy 81 GlyValAlaValAlaAspLeuPheGlnAsnLeuSerLeuIleLeuGluHisIleGluArg 100  
Db 342 GGGAGGCTGTGATTAACATTTCTCAAACTGTCTTTATTAAGAACAATAGAGCGC 283  
Qy 101 GluLeuLeuAspGlyAlaGlyGluArgTyrArgValThrIlePheLeuAspTyrLeuGln 120  
Db 282 CAATAAAGAGTGTGACAGAGAAAGATGAGAGTGAACAAGTTCTTAGACTACTGCA 223  
Qy 121 ValPheLeuGlyValIleAsnThrGluThrProGluSer 134  
Db 222 GTATTCTTGCTGTATTAACACCGAGTGAACCCGAAAGT 181  
RESULT 12  
LOCUS AR254492 610 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 80 from patent US 6482403.

ACCESSION AR254492  
 VERSION AR254492.1 GI:27303380  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCES 1 (bases 1 to 610)  
 AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
 TITLE Caniney IL-13 immunoregulatory proteins and uses thereof  
 JOURNAL Patent: US 6482403-A 80-19-NOV-2002;  
 FEATURES  
 source  
 1. 610  
 /organism="unknown"  
 /mol\_type="genomic DNA"

## ORIGIN

## Alignment Scores:

Pred. No.:	2,13e-75	Length:	610
Score:	696.00	Matches:	134
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-787-382-5 (1-134) x AR254492 (1-610)

QY 1 MetArgMetLeuLeuLeuSerLeuLeuAlaLeuGlyAlaAlaIyValSerAlaPhe 20  
 DB 29 ATGAGAAATGCTTCGAAATTTGAGTTGCTAGCTCTGGGCTGCTATGTTTCTGCCTT 88  
 QY 21 AlAlaValGluAnPromeCAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThiS 40  
 DB 89 GCTGTAGAAATATCCAGAAATAGACTGTGCGACAGACCTTGACACTGCTCTCCACTCAT 148  
 QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLyAsnHis 60  
 DB 149 CGAATCTGGCTGATAGGCGAGACCTGATGATTCCTACTCTGAAATATTAATACAC 208  
 QY 61 GlnLeuCyAllelyGluValPheGlnGlyIleAspThrLeuLyAsnGlnThrAlaHis 80  
 DB 209 CAACGTGCACTTAAAGAAATTTTACAGGTATAGACACATTGAAGAACCAAACTGCCAC 268  
 QY 81 G1yGluAlaValAlaPlyLeuPheGlnAsnLeuSerLeuIlelyGluHisIleGluArg 100  
 DB 269 GGGAGGCTGTGATTAACATTTCCAAACTTCTTATATTAAGAACACATAGAGCGC 328  
 QY 101 GlnLyLyAsnArgCysAlaGlyGluArgTrpArgValThrLyPheLeuAspTyrLeuGln 120  
 DB 329 CAAAAAAGGTGTGCGAGGAAGATGAGAGTGAACAAAGTTCCTAGACTTACCTGCA 388  
 QY 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
 DB 389 GTATTTCTTGCTATTAACACCGAGTGAACCGGAAAGT 430

## RESULT 13

AR254493/c AR254493 610 bp DNA linear PAT 20-DEC-2002  
 LOCUS Sequence 82 from patent US 6482403.  
 DEFINITION AR254493  
 ACCESSION AR254493  
 VERSION AR254493.1 GI:27303381  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCES 1 (bases 1 to 610)  
 AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
 TITLE Caniney IL-13 immunoregulatory proteins and uses thereof  
 JOURNAL Patent: US 6482403-A 82-19-NOV-2002;  
 FEATURES  
 source  
 1. 610  
 /organism="unknown"  
 /mol\_type="genomic DNA"

## ORIGIN

## Alignment Scores:

Pred. No.:	2,13e-75	Length:	610
Score:	696.00	Matches:	134
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-787-382-5 (1-134) x AR254493 (1-610)

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 QY 21 AlAlaValGluAnPromeCAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThiS 40  
 DB 522 GCTGTAGAAATATCCAGAAATAGACTGTGCGACAGACCTTGACACTGCTCTCCACTCAT 463  
 QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLyAsnHis 60  
 DB 462 CGAATCTGGCTGATAGGCGAGACCTGATGATTCCTACTCTGAAATATTAATACAC 403  
 QY 61 GlnLeuCyAllelyGluValPheGlnGlyIleAspThrLeuLyAsnGlnThrAlaHis 80  
 DB 402 CAACGTGCACTTAAAGAAATTTTACAGGTATAGACACATTGAAGAACCAAACTGCCAC 343  
 QY 81 G1yGluAlaValAlaPlyLeuPheGlnAsnLeuSerLeuIlelyGluHisIleGluArg 100  
 DB 342 GGGAGGCTGTGATTAACATTTCCAAACTTCTTATATTAAGAACACATAGAGCGC 283  
 QY 101 GlnLyLyAsnArgCysAlaGlyGluArgTrpArgValThrLyPheLeuAspTyrLeuGln 120  
 DB 282 CAAAAAAGGTGTGCGAGGAAGATGAGAGTGAACAAAGTTCCTAGACTTACCTGCA 223  
 QY 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
 DB 222 GTATTTCTTGCTATTAACACCGAGTGAACCGGAAAGT 181

## RESULT 14

AR300436 AR300436 405 bp DNA linear PAT 12-JUN-2003  
 LOCUS Sequence 1 from patent US 6537781.  
 DEFINITION AR300436  
 ACCESSION AR300436  
 VERSION AR300436.1 GI:31687875  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCES 1 (bases 1 to 405)  
 AUTHORS Guo,H., Lawton,R., Mermer,B. and Aiyappa,A.P.  
 TITLE Methods and compositions concerning canine interleukin 5  
 JOURNAL Patent: US 6537781-A 1 25-MAR-2003;  
 FEATURES  
 source  
 1. 405  
 /organism="unknown"  
 /mol\_type="genomic DNA"

## ORIGIN

## Alignment Scores:

Pred. No.:	1,61e-74	Length:	405
Score:	687.00	Matches:	133
Percent Similarity:	99.25%	Conservative:	0
Best Local Similarity:	99.25%	Mismatches:	1
Query Match:	98.71%	Indels:	0
DB:	6	Gaps:	0

US-10-787-382-5 (1-134) x AR300436 (1-405)

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 DB 1 ATGAGAAATGCTTCGAAATTTGAGTTGCTAGCTCTGGGCTGCTATGTTTCTGCCTT 60

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Qy 21 AlavaIGluAenPromeAasnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
Db 61 GCTGTAGAAAATCCCATGAAATAGACTGTGTGGCAGAGACTTGACATGCTCTCCATCAT 120
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAenLysAsnHis 60
Db 121 CGAAGCTGGCTGATAGGCGATGGGAACTGATGATTCCTACTCTGTAATAAAGAACAC 180
Qy 61 GluLeuCyHisIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80
Db 181 CAACGTGCATTAAGAAAGATTTCACAGGCTTAGACACATTTGAAGAACCAACCTGCCAC 240
Qy 81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
Db 241 GGGAGGCTGTGATTAACCTATTCCAAACTTGCTTAATAAAGAACACATGAGCGC 300
Qy 101 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
Db 301 CAAAAAAGGTGTGCAGAGAAAGATGAGAGTGAACAAAGTTCCTAGACTACTGCA 360
Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
Db 361 GTATTCTTGCTGTATTAACACCGAGTGCACATGGAAGT 402

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RESULT 15
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LOCUS AX083939
DEFINITION Sequence 1 from Patent WO0111049.
ACCESSION AX083939
VERSION AX083939.2 GI:14532940
KEYWORDS
SOURCE
ORGANISM
Canis familiaris (dog)
Canis familiaris
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Pisces; Canidae; Canis.
REFERENCE
1 Guo, H., Lawton, R., Mermer, B. and Aiyappa, A. P.
AUTHORS Methods and compositions concerning canine interleukin 5
TITL Patent: WO 0111049-A 1 15-FEB-2001;
JOURNAL IDEXX LABORATORIES, INC. (US)
COMMENT On Jun 24, 2001 this sequence version replaced gi:13185501.
FEATURES
Location/Qualifiers
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/organism="Canis familiaris"
/mol_type="unassigned DNA"
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## ORIGIN

## Alignment Scores:

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Pred. No.: 1.61e-74 Length: 405
Score: 687.00 Matches: 133
Percent Similarity: 99.25% Conservative: 0
Best Local Similarity: 99.25% Mismatches: 1
Query Match: 98.71% Indels: 0
DB: 6 Gaps: 0

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US-10-787-382-5 (1-134) x AX083939 (1-405)

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Qy 1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaIleTyrValSerAlaPhe 20
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Qy 21 AlavaIGluAenPromeAasnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
Db 61 GCTGTAGAAAATCCCATGAAATAGACTGTGTGGCAGAGACTTGACATGCTCTCCATCAT 120
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAenLysAsnHis 60
Db 121 CGAAGCTGGCTGATAGGCGATGGGAACTGATGATTCCTACTCTGTAATAAAGAACAC 180
Qy 61 GluLeuCyHisIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80
Db 181 CAACGTGCATTAAGAAAGATTTCACAGGCTTAGACACATTTGAAGAACCAACCTGCCAC 240

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Qy 81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
Db 241 GGGAGGCTGTGATTAACCTATTCCAAACTTGCTTAATAAAGAACACATGAGCGC 300
Qy 101 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
Db 301 CAAAAAAGGTGTGCAGAGAAAGATGAGAGTGAACAAAGTTCCTAGACTACTGCA 360
Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
Db 361 GTATTCTTGCTGTATTAACACCGAGTGCACATGGAAGT 402

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Search completed: August 6, 2005, 22:43:05  
Job time : 2465.9 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus2 model

Run on: August 6, 2005, 19:27:15 ; Search time 366.482 Seconds

(without alignments)  
2164.487 Million cell updates/sec

Title: US-10-787-382-5

Perfect score: 696  
Sequence: 1 MRMLNLSLALGAAVYSAF.....FLDYLYQVFLGVINTEWTPES 134

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-NO MMAP -LARGEOUDRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -MANY TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_16Dec04:

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10: geneseq2003cs:\*  
11: geneseq2003ds:\*  
12: geneseq2004as:\*  
13: geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	Score	Match	Length	ID	Description
No.						
1	696	100.0	402	3	AAZ55548	Canine in
2	696	100.0	402	3	AAZ55549	Canine in
3	696	100.0	610	3	AAZ55546	Canine in
4	696	100.0	610	3	AAZ55547	Canine in
5	687	98.7	405	4	AAZ74300	Canine in

C	6	610	87.6	345	3	AAZ55550	AAZ55550 Canine ma
	7	610	87.6	345	3	AAZ55551	AAZ55551 Canine ma
	8	591	84.9	838	3	AAZ44265	AAZ44265 Porcine I
	9	541	77.7	520	2	AAT50755	AAT50755 Ovine IL-
	10	536	77.0	399	4	AAT50756	AAT50756 Ovine IL-
	11	513	73.7	393	4	AAZ74306	AAZ74306 Canine in
	12	430	61.8	816	3	AAA34857	AAA34857 Human ade
	13	430	61.8	816	3	AAA13338	AAA13338 Human int
	14	430	61.8	816	3	AAZ20979	AAZ20979 Human low
	15	430	61.8	816	10	ADG33104	ADG33104 Human DNA
	16	430	61.8	816	10	ABZ26673	ABZ26673 Human nuc
	17	430	61.8	816	10	ACF63368	ACF63368 Human int
	18	430	61.8	816	13	ADP56009	ADP56009 Human PRO
	19	430	61.8	858	9	AAZ61293	AAZ61293 hIL5-P2-P
	20	430	61.8	858	9	AAZ61294	AAZ61294 hIL5-P30-
	21	430	61.8	4057	3	AAA34858	AAA34858 Human ade
	22	430	61.8	4057	3	AAZ20980	AAZ20980 Human low
	23	430	61.8	4057	10	ABZ26674	ABZ26674 Human nuc
	24	430	61.8	4057	11	ABD20523	ABD20523 Human pul
	25	430	61.8	4057	11	ABD20522	ABD20522 Human pul
	26	429	61.6	252	4	AAZ74305	AAZ74305 Canine in
	27	424	60.9	816	11	ADJ31910	ADJ31910 Human CDN
	28	420	60.3	402	1	AAZ81380	AAZ81380 A human B
	29	415.5	59.7	864	9	AAZ61296	AAZ61296 hIL5.37 v
	30	413.5	59.4	864	9	AAZ61295	AAZ61295 hIL5.36 v
	31	376	54.0	399	2	AAZ64061	AAZ64061 T cell re
	32	376	54.0	402	2	AAT14921	AAT14921 T cell re
	33	376	54.0	1534	2	AAT88013	AAT88013 Murine in
	34	376	54.0	1623	2	AAT14925	AAT14925 T cell re
	35	376	54.0	1623	2	AAV64062	AAV64062 Plasmid P
	36	375	53.9	1533	1	AAZ82431	AAZ82431 B cell di
	37	361	51.9	370	1	AAZ91647	AAZ91647 Synthetic
	38	361	51.9	1945	10	ADB53890	ADB53890 Primary r
	39	355	51.0	481	1	AAZ80461	AAZ80461 Clone 115
	40	351	50.4	377	2	AAV01595	AAV01595 Human int
	41	347	49.9	348	2	AAT14922	AAT14922 T cell re
	42	346	49.7	385	3	AAA43842	AAA43842 Human sec
	43	342	49.3	342	2	AAT14923	AAT14923 T cell re
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#### ALIGNMENTS

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XX	AAZ55548;
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AC	14-MAR-2000 (first entry)
XX	
DT	Canine interleukin-5 (IL-5) cDNA coding region.
XX	
DB	Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
XX	immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
KW	
KX	Canis familiaris.
OS	
XX	
XX	MO9961618-A2.
PN	
XX	02-DEC-1999.
PD	
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XX	28-MAY-1999; 99W0-US011942.
PF	
XX	29-MAY-1998; 98US-0087306P.
PR	
XX	
PA	(HESK-) HESKA CORP.
XX	
XX	Sim G, Yang S, Dretz MJ, Wonderling RS;
PI	WPI; 2000-072623/06.
XX	
DR	P-PSDB; AAY56219.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs.  
PT Useful for treating or preventing e.g. tumors or autoimmune disease.  
XX  
XX Claim 1h; Page 225; 264pp; English.  
XX  
CC Sequences AA255546-255551 represent cDNA sequences encoding canine  
CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
CC feline IL-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
CC ligand), canine IL-5, canine IL-13, feline interferon- $\alpha$  (IFN- $\alpha$ ), and  
CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
CC nucleotides which encode these immunoregulatory proteins. The proteins,  
CC their associated nucleic acids, specific antibodies and inhibitors may be  
CC used as vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans). They  
CC may be used to treat autoimmune or infectious diseases including  
CC allergies, tumors, inflammation and graft rejection, and to increase the  
CC response from a co-administered antigen. The nucleotide sequences can  
CC also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for modulators  
CC of activity, while the antibodies may be used in detection, and in drug  
CC targeting  
XX  
SQ Sequence 402 BP; 129 A; 79 C; 93 G; 101 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 7.02e-79 Length: 402  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-10-787-382-5 (1-134) x AA255548 (1-402)  
QY 1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTYrValSerAlaPhe 20  
Db 1 ATGAGAAATGCTTGAATTGAGTTTGTAAGTCTGGGGCTGCTAATGTTTGGCTTT 60  
QY 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
Db 61 GCTGTAAAGAAATCCCATGAAATAGACTGGTGGCAAGACCTTGAACATGCTCTCCACATCAT 120  
QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsnHis 60  
Db 121 CGAACTTGCTGATAGGCGATGGGAACCTGATGATCTTCTCTGAAAAATTAATTAATCAC 180  
QY 61 GluLeuCySilelysgluValPheGlnGlyIleAspThrLeuLeuAsnGlnThrAlaHis 80  
Db 181 CAACGTGCAATTAAGAAGATTTTCAAGGATATAGACATTAAGAAGAACCAATGCCCCAC 240  
QY 81 GlyGluAlaValAlaAspIleuPheGlnAsnLeuSerLeuIlelysgluHisIleGluArg 100  
Db 241 GGGGAGGCTGGATTAACATATCTCCAAAATGCTTTAAATTAAGAACACATGAGAGGC 300  
QY 101 GlnIlelysgATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
Db 301 CAAATAAAAGAGTGTGCGAGGAAGATGAGAGTGAACAAAGTTCTTGAAGTCTTGAAGTCTTGA 360  
QY 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
Db 361 GTATTTCTTGGTGTATTAACACCGAGTGAACCGGAAAGT 402  
RESULT 2  
AAZ55549/c  
ID AAZ55549 standard; cDNA; 402 BP.  
XX  
AC AAZ55549;  
XX  
DT 14-MAR-2000 (first entry)  
XX

DE Canine interleukin-5 (IL-5) cDNA coding region complement.  
XX  
XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
XX Canis familiaris.  
XX  
XX WO9961618-A2.  
XX  
XX 02-DEC-1999.  
XX  
XX 28-MAY-1999; 99WO-US011942.  
XX  
XX 29-MAY-1998; 98US-0087306P.  
XX  
XX (HESK-) HESKA CORP.  
XX  
XX Slim G, Yang S, Dretz MJ, Wonderling RS;  
XX  
XX WPI; 2000-072623/06.  
XX  
XX P-PSDB; AAY58219.  
XX  
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
XX useful for treating or preventing e.g. tumors or autoimmune disease.  
XX  
XX Claim 1h; Page 226; 264pp; English.  
XX  
XX  
CC Sequences AA255546-255551 represent cDNA sequences encoding canine  
CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
CC feline IL-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
CC ligand), canine IL-5, canine IL-13, feline interferon- $\alpha$  (IFN- $\alpha$ ), and  
CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
CC nucleotides which encode these immunoregulatory proteins. The proteins,  
CC their associated nucleic acids, specific antibodies and inhibitors may be  
CC used as vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans). They  
CC may be used to treat autoimmune or infectious diseases including  
CC allergies, tumors, inflammation and graft rejection, and to increase the  
CC response from a co-administered antigen. The nucleotide sequences can  
CC also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for modulators  
CC of activity, while the antibodies may be used in detection, and in drug  
CC targeting  
XX  
SQ Sequence 402 BP; 101 A; 93 C; 79 G; 129 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 7.02e-79 Length: 402  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-10-787-382-5 (1-134) x AA255549 (1-402)  
QY 1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTYrValSerAlaPhe 20  
Db 402 ATGAGAAATGCTTGAATTGAGTTTGTAAGTCTGGGGCTGCTAATGTTTGGCTTT 343  
QY 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
Db 342 GCTGTAAAGAAATCCCATGAAATAGACTGGTGGCAAGACCTTGAACATGCTCTCCACATCAT 283  
QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsnHis 60  
Db 282 CGAACTTGCTGATAGGCGATGGGAACCTGATGATCTTCTCTGAAAAATTAATTAATCAC 223  
QY 61 GluLeuCySilelysgluValPheGlnGlyIleAspThrLeuLeuAsnGlnThrAlaHis 80  
Db 222 CAACGTGCAATTAAGAAGATTTTCAAGGATATAGACATTAAGAAGAACCAATGCCCCAC 163

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Oy 81 G|G|U|A|A|V|A|A|P|L|Y|S|L|E|U|P|H|E|G|I|N|A|S|N|L|E|U|S|E|I|L|E|Y|G|U|H|I|E|G|U|A|G 100
Db 162 GGGGAGGCTGTGATTAACCTATTCCTTCAAACTTGTCTTAAATAAAGAACCTAAGAGGC 103
Oy 101 Glnylslysaargcyaa|ag|ygluargtrpargvalthrlyspheleuasp|tyr|leu|gln 120
Db 102 CAAAAAAGAGTGTGACGAGAAAGATGAGAGTGA|CAA|GTTCTTACTTACTGCA 43
Oy 121 ValPheleu|g|y|Val|leas|n|Thr|g|U|T|P|Thr|Pro|G|U|Ser 134
Db 42 GTATTCTTGTGTATTAATTAACACCGATGACACCGAAAGT 1
RESULT 3
AAZ55546
AAZ55546 standard; cDNA, 610 BP.
AC AAZ55546;
XX 14-MAR-2000 (first entry)
XX 14-MAR-2000 (first entry)
XX Canine interleukin-5 (IL-5) cDNA.
XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX Canis familiaris.
XX Key Location/Qualifiers
XX CDS 29..433
XX /*tag= a
XX /*product= "Canine IL-5"
XX MO9961618-A2.
XX 02-DEC-1999.
XX PD 28-MAY-1999; 99WO-US011942.
XX PF 29-MAY-1998; 98US-0087306P.
XX PR (HESK-) HESKA CORP.
XX PA
XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
XX DR P-PSDB; AAY58219.
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease.
XX Claim 1h; Page 223-224; 264pp; English.
XX Sequences AAZ55546-255551 represent cDNA sequences encoding canine
XX interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
XX feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
XX ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
XX and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
XX nucleotides which encode these immunoregulatory proteins. The proteins,
XX and their associated nucleic acids, specific antibodies and inhibitors may be
XX used as vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans). They
XX may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase the
XX response from a co-administered antigen. The nucleotide sequences can
XX also be used for the recombinant production of a protein, while
XX nucleotide fragments are useful as probes, as amplification primers and
XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX The proteins may be used to raise antibodies and to screen for modulators
XX of activity, while the antibodies may be used in detection, and in drug
XX targeting
XX Sequence 610 BP; 202 A; 114 C; 139 G; 155 T; 0 U; 0 Other;
XX SQ
```

```
Alignment Scores:
Pred. No.: 1.26e-78 Length: 610
Score: 696.00 Matches: 134
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-787-382-5 (1-134) x AAZ55546 (1-610)
Oy 1 MetArgMetLeu|Leu|Asn|Leu|Ser|Leu|Leu|Val|Leu|G|Val|Ala|Yr|Val|Ser|Ala|Phe 20
Db 29 ATGAGAAATGCTTCTGAAATTTGAGTTTGCTACTCTTGCGGCTGCTATGTTTCTGCGCTTT 88
Oy 21 AlAValG|U|A|S|N|P|P|O|M|E|T|A|S|N|A|R|G|L|E|U|V|A|L|A|G|U|T|H|R|L|E|U|S|E|T|H|I|S 40
Db 89 GCTGTAGAAATCCCATGAAATAGACTGTGTGCAGAGACCTTGACACCTGCTCCACTCAT 148
Oy 41 ArgThrT|P|Leu|I|I|G|Y|A|S|P|G|Y|A|S|N|L|E|U|S|E|I|L|E|Y|G|U|H|I|E|G|U|A|G 60
Db 149 CGAACTTGCTGATAGGCGATGGAGAACCTGATGATTTCTTACTCTTGAAATAAATAATCAC 208
Oy 61 Glnleu|Cy|I|e|y|S|G|I|U|V|A|P|H|E|G|I|N|G|Y|I|L|E|A|S|P|T|H|R|L|E|U|Y|A|S|N|G|I|N|T|H|A|H|I|S 80
Db 209 CAACGTGCACTTAAGAAGATTTTCAAGGTATAGACACATTTGAAGAACCAACGCGCCAC 268
Oy 81 G|Y|G|U|A|A|V|A|A|P|L|Y|S|L|E|U|P|H|E|G|I|N|A|S|N|L|E|U|S|E|I|L|E|Y|G|U|H|I|E|G|U|A|G 100
Db 269 GGGGAGGCTGTGATTAACCTATTCCTTCAAACTTGTCTTAAATAAAGAACACATAGAGCGC 328
Oy 101 Glnylslysaargcyaa|ag|ygluargtrpargvalthrlyspheleuasp|tyr|leu|gln 120
Db 329 CAAAAAAGAGTGTGACGAGAAAGATGAGAGTGA|CAA|GTTCTTACTTACTGCA 388
Oy 121 ValPheleu|g|y|Val|leas|n|Thr|g|U|T|P|Thr|Pro|G|U|Ser 134
Db 389 GTATTCTTGTGTATTAATTAACCGAGTGA|CAA|GTTCTTACTTACTGCA 430
RESULT 4
AAZ55547/C
AAZ55547 standard; cDNA, 610 BP.
AC AAZ55547;
XX 14-MAR-2000 (first entry)
XX 14-MAR-2000 (first entry)
XX Canine interleukin-5 (IL-5) cDNA complement.
XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX Canis familiaris.
XX Key Location/Qualifiers
XX CDS 178..582
XX /*tag= a
XX /*product= "Canine IL-5"
XX MO9961618-A2.
XX 02-DEC-1999.
XX PD 28-MAY-1999; 99WO-US011942.
XX PF 29-MAY-1998; 98US-0087306P.
XX PR (HESK-) HESKA CORP.
XX PA
XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
XX DR P-PSDB; AAY58219.
XX SQ
```

XX Nucleic acid encoding immunoregulatory proteins from cats or dogs.  
PT useful for treating or preventing e.g. tumors or autoimmune disease.  
XX  
PS Claim 1h; Page 224-225; 264pp; English.

XX Sequences AA255546-255551 represent cDNA sequences encoding canine  
CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
CC nucleotides which encode these immunoregulatory proteins. The proteins,  
CC their associated nucleic acids, specific antibodies and inhibitors may be  
CC used as vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans). They  
CC may be used to treat autoimmune or infectious diseases including  
CC allergies, tumors, inflammation and graft rejection, and to increase the  
CC response from a co-administered antigen. The nucleotide sequences can  
CC also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for modulators  
CC of activity, while the antibodies may be used in detection, and in drug  
CC targeting.

XX SQ Sequence 610 BP; 155 A; 139 C; 114 G; 202 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	1,26e-78	Length:	610
Score:	696.00	Matches:	134
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-787-382-5 (1-134) x AA255547 (1-610)

```
QY 1 MetArgMetLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaTyValSerAlaPhe 20
Db 582 ATGAGAAATGCTTGAATTGAGTTTGCTAGCTCTGGGGCTGCTAATGTTTGCCTTT 523
QY 21 AlAlaIGluAenProMetAenAArgLeuValAlaGluThrLeuThrLeuLeuSerThHis 40
Db 522 GCTGTAGAAAATCCCAAGAAATAGACTGTGTGCAGACCTTGAACATGCTCTCCACATCAT 463
QY 41 ArgThrTrpLeuIleGlyAaSPGlyAaenLeuMetIleProThrProGluAaenLyAaenHis 60
Db 462 CGAACTTGCTGATAGCGAGTGGAACTGATGATCTTCTACTCTGAAAAATAAAAATCAC 403
QY 61 GlnLeuCySilelySgiuValPheGlnGlyIleAaSPThrLeuLySaaenGlnThrAlaHis 80
Db 402 CAACGTGACATTAAGAAGATTTCAGGGTATAGACATTAAGAAGAACCAAGCCAC 343
QY 81 GlyGluAlaValAlaPlySleuPheGlnAaenLeuSerLeuIlelySgiuHisIleGluArg 100
Db 342 GGGAGGCTGTGATAACTAATTCCTGCTTAAATTAAGAAGAACATAGAGCGC 283
QY 101 GlnlySlyAaRGCySAlaGlyGlyArgTrpArgValThrlySPhelAaSPTyRLeuGln 120
Db 282 CAAAAAAGAGGTGTGCGAGGAAGATGAGAGTGAAGAACTTCTAGACTTACTGCA 223
QY 121 ValPheLeuGlyValIleAaenThrGluTrpThrProGluSer 134
Db 222 GTATTTCTTGSTGTATTAACACCGAGTGACACCGAAGT 181
```

#### RESULT 5

AAAF74300 standard; DNA; 405 BP.

XX AAFA74300;

XX 04-MAY-2001 (first entry)

DE Canine interleukin-5 coding sequence #1.  
XX Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;  
KM inflammatory reaction; ds.  
XX  
OS Canis sp.

XX PN WO200111049-A2.  
XX 15-FEB-2001.

XX PD 09-AUG-2000; 2000WO-US021651.

XX PR 10-AUG-1999; 99US-00372615.

XX PA (IDEX-) IDEXX LAB INC.

XX PI Guo H, Lawton R, Mermer B, Alayappa AP;

XX DR WPI; 2001-191542/19.

XX DR P-PSDB; AAB72615.

XX PT Novel canine interleukin 5 polynucleotide and polypeptides are used for  
PT generating antibodies which are useful in treating allergies in dogs.

XX PS Claim 31; Page 46; 48pp; English.

XX The present invention provides the protein and coding sequences of the  
CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,  
CC cancer and inflammatory reactions in dogs. The present sequence is one  
XX version of the IL-5 coding sequence shown in the specification

XX SQ Sequence 405 BP; 131 A; 77 C; 94 G; 103 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	9,89e-78	Length:	405
Score:	687.00	Matches:	133
Percent Similarity:	99.25%	Conservative:	0
Best Local Similarity:	99.25%	Mismatches:	1
Query Match:	98.71%	Indels:	0
DB:	4	Gaps:	0

US-10-787-382-5 (1-134) x AAFA74300 (1-405)

```
QY 1 MetArgMetLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaTyValSerAlaPhe 20
Db 1 ATGAGAAATGCTTGAATTGAGTTTGCTAGCTCTGGGGCTGCTAATGTTTGCCTTT 60
QY 21 AlAlaIGluAenProMetAenAArgLeuValAlaGluThrLeuThrLeuLeuSerThHis 40
Db 61 GCTGTAGAAAATCCCAAGAAATAGACTGTGTGCAGAGACCTTGAACATGCTCTCCACATCAT 120
QY 41 ArgThrTrpLeuIleGlyAaSPGlyAaenLeuMetIleProThrProGluAaenLyAaenHis 60
Db 121 CGAACTTGCTGATAGCGAGTGGAACTGATGATCTTCTACTCTGAAAAATAAAAATCAC 180
QY 61 GlnLeuCySilelySgiuValPheGlnGlyIleAaSPThrLeuLySaaenGlnThrAlaHis 80
Db 181 CAACGTGACATTAAGAAGATTTCAGGGTATAGACATTAAGAAGAACCAAGCCAC 240
QY 81 GlyGluAlaValAlaPlySleuPheGlnAaenLeuSerLeuIlelySgiuHisIleGluArg 100
Db 241 GGGAGGCTGTGATAACTAATTCCTGCTTAAATTAAGAAGAACATAGAGCGC 300
QY 101 GlnlySlyAaRGCySAlaGlyGlyArgTrpArgValThrlySPhelAaSPTyRLeuGln 120
Db 301 CAAAAAAGAGGTGTGCGAGGAAGATGAGAGTGAAGAACTTCTAGACTTACTGCA 360
QY 121 ValPheLeuGlyValIleAaenThrGluTrpThrProGluSer 134
Db 361 GTATTTCTTGSTGTATTAACACCGAGTGACACCGAAGT 402
```

#### RESULT 6



AAZ5550  
ID AAZ5550 standard; cDNA; 345 BP.  
XX  
AC AAZ5550;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-5 (IL-5) cDNA.  
XX  
KM Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
KM Immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
EN MO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US011942.  
XX  
PR 29-MAY-1998; 98US-0087306P.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; AAY58220.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease.  
XX  
PS Claim 1h; Page 226-227; 264pp; English.  
XX  
CC Sequences AAZ55546-255551 represent cDNA sequences encoding canine  
CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
CC nucleotides which encode these immunoregulatory proteins. The proteins,  
CC their associated nucleic acids, specific antibodies and inhibitors may be  
CC used as vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans). They  
CC may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase the  
CC response from a co-administered antigen. The nucleotide sequences can  
CC also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for modulators  
CC of activity, while the antibodies may be used in detection, and in drug  
CC targeting.  
XX  
SQ Sequence 345 BP; 120 A; 68 C; 78 G; 79 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 4.85e-68 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservatve: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 87.64% Indels: 0  
DB: 3 Gaps: 0  
US-10-787-382-5 (1-134) x AAZ55550 (1-345)  
Qy 20 PheAAValaGluAenProMetAsnArgLeuValaIaGluTrpLeuThrLeuLeuSerThr 39  
Db 1 TTCTGCTGAGAAATCCCATGATGACTGTGGAGAGACTTACACCTGCTCCACT 60  
Qy 40 HisArgThrTrpLeuIleGlyAspGlyAsnLeuNecIleProThrProGluAsnLysAn 59  
Db 61 CATGGAACCTGGCTGATAGCGAGATGGAACTGATGATCTTACTCTGAAATAATAAT 120

Qy 60 HisGlnLeuCyelIeYgIuValPheGlnGlyIleAepThrLeuLysAsnGlnThrAla 79  
Db 121 CACCACTGTCATTAAGAAAGTTTTCAGGGTATAGACATTCGAAACCAACTGCC 180  
Qy 80 HisGlyGluValaValaLeuPheGlnAsnLeuSerIleIleYgIuHisIleGlu 99  
Db 181 CACGGGAGGCTGTGATTAACCTATTCGAAACCTTGTCTTAATTAAGAACACATAGAG 240  
Qy 100 ArgGlnLysValaGlyGlyIleGluValaGlyTrpArgValaThrLysPheLeuAspTrpLeu 119  
Db 241 CGCCAAAAAAGAGTGTGCGAGAGAAAGAGAGAGTGAACAAAGTCTCTAGACTACTG 300  
Qy 120 GlnValPheLeuGlyValaIleAsnThrGluTrpThrProGluSer 134  
Db 301 CAGTATTTCTTGATGATTAACACCGAGTGGACACCGGAAAGT 345  
RESULT 7  
AAZ5551/C  
ID AAZ5551 standard; cDNA; 345 BP.  
XX  
AC AAZ5551;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-5 (IL-5) cDNA complement.  
XX  
KM Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
KM Immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
EN MO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US011942.  
XX  
PR 29-MAY-1998; 98US-0087306P.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; AAY58220.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease.  
XX  
PS Claim 1h; Page 228; 264pp; English.  
XX  
CC Sequences AAZ55546-255551 represent cDNA sequences encoding canine  
CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
CC nucleotides which encode these immunoregulatory proteins. The proteins,  
CC their associated nucleic acids, specific antibodies and inhibitors may be  
CC used as vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans). They  
CC may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase the  
CC response from a co-administered antigen. The nucleotide sequences can  
CC also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for modulators  
CC of activity, while the antibodies may be used in detection, and in drug  
CC targeting.  
XX  
SQ Sequence 345 BP; 79 A; 78 C; 68 G; 120 T; 0 U; 0 Other;  
XX  
Alignment Scores:

Pred. No.: 4,85e-68 Length: 345  
 Score: 610.00 Matches: 115  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 87.64% Indels: 0  
 DB: 3 Gaps: 0

US-10-787-382-5 (1-134) x AA255551 (1-345)

Qy 20 PheAlaValGluAnPromeAAsnArgLeuValAlaGluThrLeuThrLeuSerThr 39  
 Db 345 TTTCGTGAGAAATCCCATATATAGACTGTGGCAGAGACCTTGACACTGCTCCACT 286  
 Qy 40 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleAsn 59  
 Db 285 CATGAACTTGCTGATAGGCGATGGGAACTGTATGATCTTACTCTGAAAAATAAAAAT 226  
 Qy 60 HisGlnLeuCySllleYsGluValPheGlnGlyIleAspThrLeuIleAsnGlnThrAla 79  
 Db 225 CACCACTGTGCATTAAAGAAAGTTTTCAGGGTATAGCACATTGAAGAACCAACCTGCC 166  
 Qy 80 HisGlnGluAlaValAspLeuLeuPheGlnAsnLeuSerIleIleYsGlnHisIleGlu 99  
 Db 165 CACGGAGAGCTGTGATTAACCTATTCCTTAAATTAAGAACACATAGAG 106  
 Qy 100 ArgGlnIleYsAsnGlyAsnGlyValGlyIleArgTrpArgValThrIleYsPheLeuAspTrpLeu 119  
 Db 105 CGCCAAAAAAGAGTGTGCGAGAAAGATGGAAGTGAACAAAGTCTTACCTGACTG 46  
 Qy 120 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
 Db 45 CAAGTATTTCTGTGTATTAACACCGAGTGAACCGGAAAGT 1

# RESULT 8

AA244265 standard; DNA; 838 BP.

AA244265;

31-MAR-2000 (first entry)

Porcine IL-5 DNA.

Pig; vaccine; cysticercosis; protective antigen; cCl; cC3; cC4;

central cysticercus; gamma interferon; IFN-gamma; interleukin 5; IL-5; ss.

Sus scrofa.

CNI231339-A.

13-OCT-1999.

29-JAN-1999; 99CN-00113447.

29-JAN-1999; 99CN-00113447.

(UTM-) UNIV NO 2 MILITARY MEDICAL PLA.

Sun S, Dai J;

WPI; 2000-087904/08.

Nucleic acid vaccine for cysticercosis co-contracted by human and pig.

Claim 3; Page 9; 21pp; Chinese.

This invention describes a novel nucleic acid vaccine for preventing and curing human and pork cysticercosis. The invention involves the formation of a eukaryotic expression plasmid from fusion transcript expression unit consisting of three protective antigen genes (cCl, cC3 and cC4) of pig central cysticercus and coexpression unit of related cell factor gamma interferon (IFN-gamma) and pork interleukin 5 (IL-5) genes. The production and purification process of said nucleic acid vaccine is

CC simple and convenient, the physical and chemical properties of the  
 CC vaccine are stable, and the vaccine is easy to store and transport, and  
 CC possesses effective immunological protective function for human and pig  
 CC cysticercosis. This sequence represents the pig IL-5 gene used in the  
 CC method of the invention

SQ Sequence 838 BP; 280 A; 148 C; 171 G; 239 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 4.37e-65 Length: 838  
 Score: 591.00 Matches: 114  
 Percent Similarity: 93.28% Conservative: 11  
 Best Local Similarity: 85.07% Mismatches: 9  
 Query Match: 84.91% Indels: 0  
 DB: 3 Gaps: 0

US-10-787-382-5 (1-134) x AA244265 (1-838)

Qy 1 MetArgMetLeuLeuAnLeuSerLeuLeuAlaIleuGlyValAlaIleValSerAlaPhe 20  
 Db 45 ATGAGAAATGCTTCTGCACTTGAATTCCTAGCTCTGGGGCTGCTATGTTCTGCCATT 104  
 Qy 21 AlaValGluAnPromeAAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40  
 Db 105 GCTGTACAAAGCTCCCATGAATAGAGCTGTGGCAGAGACCTTGGCAGCTGCTCCACTCAT 164  
 Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAnLeuYsAsnHis 60  
 Db 165 CGAAGCTTACTGATAGCGCAGCGAAGCTGATGATTCCTCTGTAACATTAACATCAC 224  
 Qy 61 GlnLeuCySllleYsGluValPheGlnGlyIleAspThrLeuIleAsnGlnThrAlaHis 80  
 Db 225 CAAGTGTGATTAAGAAAGCTTTCAGGGTATAGACACATTAAGAAATCCACACTGTGCCG 284  
 Qy 81 GlyGluAlaValAspLeuLeuPheGlnAsnLeuSerIleIleYsGlnHisIleGluArg 100  
 Db 285 GGGAGTGTGGAAGAGCTTTCGAAACTGTCTTAAATTAAGAACACATAGACCGC 344  
 Qy 101 GlnIleYsAsnGlyAsnGlyValArgTrpArgValThrIleYsPheLeuAspTrpLeuGln 120  
 Db 345 CAAAAAAGAGTGTGAGAGAAAGATGGAAGTGAACAAAGTCTTACCTGACTGCTGCA 404  
 Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
 Db 405 GTGTTCTTGTGTATTAACACCTGAGTGAACATGAAAGT 446

## RESULT 9

AAT50755 standard; DNA; 520 BP.

AAT50755;

17-OCT-2003 (revised)

24-SEP-1997 (first entry)

Ovine IL-5 gene.

Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;

livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;

immunosuppression; allergy; reproductive system; growth; early maturity;

antibody; diagnosis; immunopotentiator;

early haematopoietic progenitor cell; cytotoxic cell; thymocyte;

secretion; IGM; IGA; bacterial endotoxin; gamma-interferon; ss.

Ovis aries.

Location/Qualifiers  
 Key 46..444  
 CDS /tag= a  
 FT /product= "Ovine\_IL-5"  
 FT exon 46..183  
 FT /tag= b  
 FT /number= 1

```

FT exon 184..216
FT /tag=C
FT /number=2
FT 217..345
FT exon /tag=d
FT /number=3
FT 346..480
FT /tag=e
FT /number=4
XX
XX MO9700321-A1.
XX
XX 03-JAN-1997.
XX
XX 14-JUN-1996; 96WO-AU000360.
XX
XX 14-JUN-1995; 95AU-00003502.
XX
XX 27-OCT-1995; 95AU-00006244.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Secw H, Wood P;
XX
XX WPI; 1997-077528/07.
XX
XX P-PSDB; AAM08479.
XX
XX Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
XX adjuvants and to treat or prevent microbial infections in livestock.
XX
XX Claim 6; Page 39-40; 78pp; English.
XX
XX The sequences given in AAT50755-56 encode ovine interleukin-5 (IL-5).
XX Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
XX livestock (esp. cows and sheep), particularly where the animals are
XX stressed, e.g. during transport. IL-5 and IL-12 can also be used as
XX adjuvants in vaccines for veterinary use (partic. weakly immunogenic
XX subunit or synthetic peptide vaccines). They may also be used to treat
XX cancer, immunosuppression and allergy, to enhance/suppress the
XX reproductive system and to promote growth or early maturity. Optionally
XX interleukin can be delivered from constructs or delivery cells and
XX antibodies are useful in enzyme immunoassays for rapid diagnosis of
XX infection. The interleukins are immunopotentiators, especially IL-5
XX promotes growth of early hematopoietic progenitor cells and generation
XX of cytotoxic cells from thymocytes, also it stimulates production and
XX secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
XX induces production of gamma-interferon by, and proliferation of, T and NK
XX cells and increases the (non)-specific cytolytic lymphocyte response. The
XX genetic constructs can also be used for in vitro production of IL-5 or -
XX 12. (Updated on 17-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 520 BP; 166 A; 99 C; 124 G; 131 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 5.08e-59 Length: 520
XX Score: 541.00 Matches: 105
XX Percent Similarity: 90.23% Conservative: 15
XX Best Local Similarity: 78.95% Mismatches: 13
XX Query Match: 77.73% Indels: 0
XX Gaps: 0
XX
XX US-10-787-382-5 (1-134) x AAT50755 (1-520)
XX
XX 2 ArgMetLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaIrrValSerAlaPheAla 21
XX AGAATGCAATCTGCGCTTACCTTGAGCTCTTGAGAGCTGCTATGTTTGAGCCAAATGCT 102
XX
XX 22 ValGluAenProMetAanArgLeuValAlaGluThrLeuThrLeuLeuSerThiHisArg 41
XX GTAGAAATACCAAGAAATAGACTGTGGCAAGAGACTTGACCTCTCCACGCAATCAA 162
XX
XX 42 ThrTrrLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGln 61
XX ACTGCTGATAGAGGATGGAGAACTTGAATGATTCCTACTCCAGCAATCAAAATCACCAG 222

```

```

OY 62 LeuCySIllelysgIValIlePheGlnGlyIleAspThrLeuLysAsnGlnIThrAlaHisGly 81
.. |||||
DB 223 CTATGCAATGAAAGCTTTTCAGAGAAATACACATTTGAAGATCAACATGCCACAAAGGG 282
OY 82 GluAlaValAspIlyLeuPheGlnAsnLeuSerLeuIlelysgIWHIaIleGluArgGln 101
DB 283 GATGCTGTGAAGAAATATATTCGAAACTTGCTTTAATTAAGAAATCATGACTCCAA 342
OY 102 LysIlysaArgCySaIaGlyGluArgIrrArgValIThrIlyPheLeuAspIrrLeuGlnVal 121
DB 343 AAAAGCAAGTGTGAGAGAAAGATGAGAGTGAACAAATTCCTGCACTACCTCGAAGTT 402
OY 122 PheLeuGlyValIleAenThrGluThrProGluSer 134
DB 403 TTCCTGTGTGATTAACACAGAGTGAACGATGAAAGC 441
RESULT 10
AAT50756
ID AAT50756 standard; cDNA; 399 BP.
XX
XX AAT50756;
XX
XX 17-OCT-2003 (revised)
XX 24-SBP-1997 (first entry)
XX
XX Ovine IL-5 cDNA.
XX
XX Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
XX livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;
XX immunosuppression; allergy; reproductive system; growth; early maturity;
XX antibody; diagnosis; immunopotentiator;
XX early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
XX secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.
XX
XX Ovis aries.
XX
XX MO9700321-A1.
XX
XX 03-JAN-1997.
XX
XX 14-JUN-1996; 96WO-AU000360.
XX
XX 14-JUN-1995; 95AU-00003502.
XX
XX 27-OCT-1995; 95AU-00006244.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Secw H, Wood P;
XX
XX WPI; 1997-077528/07.
XX
XX P-PSDB; AAM08479.
XX
XX Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
XX adjuvants and to treat or prevent microbial infections in livestock.
XX
XX Claim 6; Page 41-42; 78pp; English.
XX
XX The sequences given in AAT50755-56 encode ovine interleukin-5 (IL-5).
XX Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
XX livestock (esp. cows and sheep), particularly where the animals are
XX stressed, e.g. during transport. IL-5 and IL-12 can also be used as
XX adjuvants in vaccines for veterinary use (partic. weakly immunogenic
XX subunit or synthetic peptide vaccines). They may also be used to treat
XX cancer, immunosuppression and allergy, to enhance/suppress the
XX reproductive system and to promote growth or early maturity. Optionally
XX interleukin can be delivered from constructs or delivery cells and
XX antibodies are useful in enzyme immunoassays for rapid diagnosis of
XX infection. The interleukins are immunopotentiators, especially IL-5
XX promotes growth of early hematopoietic progenitor cells and generation
XX of cytotoxic cells from thymocytes, also it stimulates production and
XX secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
XX induces production of gamma-interferon by, and proliferation of, T and NK

```

CC cells and increases the (non)-specific cytolytic lymphocyte response. The  
CC genetic constructs can also be used for in vitro production of IL-5 or -  
CC 12. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 399 BP, 130 A; 77 C; 93 G; 99 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	1,52e-58	Length:	399
Score:	536.00	Matches:	104
Percent Similarity:	90.15%	Conservative:	15
Best Local Similarity:	78.79%	Mismatches:	13
Query Match:	77.01%	Indels:	0
DB:	2	Gaps:	0

US-10-787-382-5 (1-134) x AAT50756 (1-399)

QY 3 MetleuLeuAenLseuSerleuLeuAlaLeuGlyAlaAlaTYValSerAlaPheAlaVal 22  
Db 1 ATGCATCTGCCTTGAACCTTGTAGCTCTTGAGCTGCACTGCTATGTTTGTGCCAATGCTGTA 60

QY 23 GluAspProweCaanArgLeuValAlaGluThrleuThrleuLeuSerThrAlaArgThr 42  
Db 61 GAAAGTACATGAATAGACTGTGGCAGAGACCTTGACACTGCTCCACGACCAAACT 120

QY 43 TrpleuilegIyaepGlyAsnLeuMetIleProThrProGluAsnIleAsnIleGlnLeu 62  
Db 121 CTGCTGATAGCTGATGGGAACTTGATGATTCCTACTCTCCACATCAAAATCACAACATA 180

QY 63 CyeIleIysGlyValPheGlnGlyIleAspThrleuIysAsnGlnIleAlaIleGlyGlu 82  
Db 181 TGCATGAGAGGCTTTCAGGAGATAGACATTTGAAGATCAACATGCACAAAGGGAT 240

QY 83 AlaValAspIysLeuPheGlnAsnLeuSerleuIleIysGlnIleAlaIleGlyArgGlnIlys 102  
Db 241 GCTGTGAAAAAATAATTCGAACTGTCTTTAATAAAGAAATCAATGACCTCCAAAATA 300

QY 103 LysArgCysAlaGlyIleArgTyrArgValThrIysPheLeuAspTyrLeuGlnValPhe 122  
Db 301 AGGAGGCTGAGGAGGAGGAGATGAGAGTGAACATTCCTCGACTACCTGCAAGTTTTC 360

QY 123 LeuGlyValIleAsnThrGluThrProGluSer 134  
Db 361 CTGTGTGATTAACACAGAGTGCATGGAAGGC 396

RESULT 11  
AAAF74306  
ID AAF74306 standard; DNA; 393 BP.

AC AAF74306;  
XX 04-MAY-2001 (first entry)

DE Canine interleukin-5 coding sequence #3.  
XX Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;  
KW inflammatory reaction; ds.

OS Canis sp.  
XX WO200111049-A2.

PN 15-FEB-2001.  
PD 09-AUG-2000; 2000WO-US021651.

PF 10-AUG-1999; 99US-00371615.  
PR (INDEX-) IDEXX LAB INC.

PA Guo H, Lawton R, Mermer B, Aiyappa AP;  
XX WPI; 2001-191542/19.

PT Novel canine interleukin 5 polynucleotide and polypeptides are used for  
PT generating antibodies which are useful in treating allergies in dogs.

XX Claim 1; Page 35; 48pp; English.

CC The present invention provides the protein and coding sequences of the  
CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,  
CC cancer and inflammatory reactions in dogs. The present sequence is one  
XX version of the IL-5 coding sequence shown in the specification

SO Sequence 393 BP, 128 A; 82 C; 86 G; 97 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	1.24e-55	Length:	393
Score:	513.00	Matches:	95
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	97.94%	Mismatches:	0
Query Match:	73.71%	Indels:	0
DB:	4	Gaps:	0

US-10-787-382-5 (1-134) x AAF74306 (1-393)

QY 35 ThrleuLeuSerThrAlaArgThrTrpleuIleGlyAspGlyAsnLeuMetIleProThr 54  
Db 1 AACTGCTCTCCACTCATCAACTTGACTATAGGCGAATGCGAATGATTCCTACT 60

QY 55 ProGluAsnIysAsnIleGlnLeuCyeIleIysGlnValPheGlnGlyIleAspThrLeu 74  
Db 61 CTTGAAATTAATAATCCCAACTGTGCATTAAGAAATTTTTCAGGATTAAGACAACTTG 120

QY 75 LysAsnGlnThrAlaIleGlyIleValAspIysLeuPheGlnAsnLeuSerleuIle 94  
Db 121 AAGAACCAAACTGCCCAAGGAGGCTGTGATTAACATTTCCAAACTGTCTTTATA 180

QY 95 LysGlnIleIleGlyIleValIysArgCysAlaGlyIleArgTyrArgValIleThrIys 114  
Db 181 AAGAAACATAGAGCCCAAAAAAAGGTGTGACAGAGAAATGAGAGTGAAG 240

QY 115 PheLeuAspTyrLeuGlnValPheLeuGlyValIleAsnThrGluTrpThr 131  
Db 241 TTCTTACACTACCTGCAGAGTATTTCTTGTCTATATAAACCCAGGTGAGT 291

RESULT 12  
AAA34857  
ID AAA34857 standard; DNA; 816 BP.

AC AAA34857;  
XX 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide SEQ ID NO:2546.  
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antispasmodic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.  
XX WO200009525-A2.

PN 24-FEB-2000.  
PD 03-AUG-1999; 99WO-US017712.

PF 03-AUG-1998; 98US-0095212P.  
PR (UYEC-) UNIV EAST CAROLINA.

PI Nyce JW;  
XX  
XX WPI: 2000-205971/18.  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
XX Disclosure; Page 716; 1343bp; English.  
XX  
XX The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
CC carcinomas, and cancers which may metastasize to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ON reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA3313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
XX SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;  
XX  
XX  
XX Alignment Scores:  
Pred. No.: 1,23e-44 Length: 816  
Score: 430.00 Matches: 87  
Percent Similarity: 77.61% Conservative: 17  
Best Local Similarity: 64.93% Mismatches: 30  
Query Match: 61.78% Indels: 0  
Gaps: 0  
US-10-787-382-5 (1-134) x AAA34857 (1-816)  
Qy 1 MetArgMetLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaIYValSerAlaPhe 20  
Db 45 ATGAGATGCTTCTGCAATTGAGTTTGTCTACTCTTGGAGCTGCTACGTGTATGCCATC 104  
Qy 21 AlavalGluAenPrometAenAArgLeuValAlaGluThrLeuThrLeuLeuSerThHis 40  
Db 105 CCCACAGAAATTCACACAGATGTCATGTAAGAGACTTGGACATGCTTCTTACTCAT 164  
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsnHis 60  
Db 165 CGAAGCTGCTGATAGCAATGACATGACCTGAGATTCCTGCTCTGATCAATAAATATAC 224  
Qy 61 GluLeuGlyIleLeuGlyValAlaPheGlnGlyIleAspThrLeuLeuAsnGlnThrAlaHis 80  
Db 225 CAATCTGACCTGAAGAAATCTTTCAGGAATAGGCACATCGAGAGTCAAACTGTGCA 284  
Qy 81 GlyGluAlaValAlaPheLeuPheGlnAsnLeuSerLeuIleGlyHisIleGluArg 100  
Db 285 GGGGGTACTGTGGAAGACTATTCAAAATCTTCTTAAATTAAGAAATATACATGACGCC 344  
Qy 101 GlnIleGlySerGlyValAlaGlyGluArgTrpArgValThrLeuPheLeuAspTyrLeuGln 120  
Db 345 CAAAAAAAAGTGTGAGAAAGAAAGACGAGAGATGAAACCAATTCCTAGACTACCTGCA 404

Qy 121 ValPheLeuGlyValIleAenThrGluTrpThrProGluSer 134  
Db 405 GAGTTCTTGTGTATGATGAACACCGAGTGCATATAGAAACT 446  
RESULT 13  
AAA13338  
ID AAA13338 standard; cDNA; 816 BP.  
XX  
XX  
XX AAA13338;  
XX  
XX 25-JUL-2000 (first entry)  
XX  
XX Human interleukin-5 (IL-5) nucleotide sequence.  
XX  
XX Human, interleukin-5; IL-5; inflammatory disease; asthma; eczema;  
KM antisense oligonucleotide; allergic rhinitis; inflammatory skin disease;  
KM allergic conjunctivitis; inhibitor; ss.  
XX  
XX Homo sapiens.  
XX  
XX US6048726-A.  
XX  
XX 11-APR-2000.  
XX  
XX 15-MAY-1998; 98US-00079839.  
XX  
XX 15-MAY-1998; 98US-00079839.  
XX  
XX (WELT/) WELTMAN J K.  
PA (KARI/) KARIM A S.  
XX  
XX WELTMAN JK, KARIM AS;  
XX  
XX WPI: 2000-302784/26.  
XX  
XX Oligonucleotide comprising non-natural internucleoside linkage, useful  
PT for inhibiting interleukin-5 expression and treating inflammatory  
PT diseases, asthma, allergic rhinitis, allergic conjunctivitis.  
XX  
XX Disclosure; Col 3-4; 11pp; English.  
XX  
XX This sequence represents the human interleukin-5 (IL-5) encoding  
CC nucleotide sequence. Interleukin-5 is involved in eosinophilic  
CC inflammation and inflammatory disorders. The present invention relates to  
CC an IL-5 antisense oligonucleotide (see AAA13337) which inhibits the  
CC expression of IL-5. The antisense oligonucleotide has at least one non-  
CC natural internucleoside linkage. The oligonucleotide is able to inhibit  
CC IL-5 secretion in a dose dependent manner, and is useful for inhibiting  
CC IL-5 expression and therefore treating inflammatory diseases, asthma,  
CC allergic rhinitis, allergic conjunctivitis and inflammatory skin diseases  
CC such as eczema  
XX  
XX SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;  
XX  
XX  
XX Alignment Scores:  
Pred. No.: 1,23e-44 Length: 816  
Score: 430.00 Matches: 87  
Percent Similarity: 77.61% Conservative: 17  
Best Local Similarity: 64.93% Mismatches: 30  
Query Match: 61.78% Indels: 0  
Gaps: 0  
US-10-787-382-5 (1-134) x AAA13338 (1-816)  
Qy 1 MetArgMetLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaIYValSerAlaPhe 20  
Db 45 ATGAGATGCTTCTGCAATTGAGTTTGTCTACTCTTGGAGCTGCTACGTGTATGCCATC 104  
Qy 21 AlavalGluAenPrometAenAArgLeuValAlaGluThrLeuThrLeuLeuSerThHis 40  
Db 105 CCCACAGAAATTCACACAGATGTCATGTAAGAGACTTGGACATGCTTCTTACTCAT 164  
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsnHis 60

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Db 165 CGAACTGCTGATGAGCAATGAGACTCTGAGGATTCCTGTTCTGTACATTAATAACAC 224
Qy 61 GlnleuCyileuysgluValpHeGlnGlyleAspHrleuysaanglnthAlHis 80
Db 225 CAATGTCGACTGAGAAATCTTTCAGGAAATAGCCACATCGAGAGCTCAAACTGTGCA 284
Qy 81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerleuileuysgluHsileGluArg 100
Db 285 GGGGGTACTGTGGAAGACTATTCAAAAACCTTGTCTTAATAAAGAAATCATTGACGGC 344
Qy 101 GlnLysLysArgCyAlaGlyGluArgTTPArgValThrLysPheLeuAspTYrLeuGln 120
Db 345 CAAAAAAGAAAGTGTGAGAAAGAAAGACGAGAGCTAAACCAATTCCTAGACTACTGCA 404
Qy 121 ValPheLeuGlyValIleAsnThrGluThrProGluSer 134
Db 405 GAGTTCTTGTTGTAATGAACACCGAGTGTAAATAGAAAGT 446

```

## RESULT 14

AAF20979  
ID AAF20979 standard; DNA, 816 BP.

AC AAF20979;

DT 14-MAR-2001 (first entry)

DE Human low adenosine antisense oligonucleotide related sequence #2546.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
XX human; airway disorder; bronchoconstriction; lung inflammation;  
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
XX immunosuppressive; antileukemic; analgesic; hypotensive; cytostatic;  
XX respiratory obstruction; pulmonary obstruction; impaired respiration;  
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
XX cancer; ss.

XX Homo sapiens.

XX MO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000MO-US008020.

XX 06-APR-1999; 99US-0127958P.

XX (UEG-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J W.

XX NYce JW;

XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
PT adenosine receptors during metabolism, useful e.g. for treating cancers  
PT and respiratory obstructions.

XX Disclosure; Page 788; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antileukemic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and/or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and

CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system peptide  
CC receptors, CNS and peripheral factors, vasoactive peptides and  
CC transmitters, defensins, growth factors, malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
CC surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impaired respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
CC fragments and antisense oligonucleotides used in the exemplification of  
CC the present invention

XX Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	Length:	Matches:	Score:
1.23e-44	816	87	430.00
Percent Similarity:	77.61%	Conservative:	17
Best Local Similarity:	64.93%	Mismatches:	30
Query Match:	61.78%	Indels:	0
DB:	3	Gaps:	0

US-10-787-382-5 (1-134) x AAF20979 (1-816)

```

Qy 1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTYrValIserAlaPhe 20
Db 45 ATGAGATGCTTGTGCAATTTGAGTTTCTAGCTTGTGAGCTGCTAGCGATGCGATG 104
Qy 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
Db 105 CCCACAGAAATGTCACCAAGTGCATGCTGTGTAAGAGACCTTGCGACCTGTTCTAC 164
Qy 41 ArgThrTrpLeuIleGlyAspArgGlyAsnLeuMetIleProThrProGluAsnLysValHis 60
Db 165 CGAACTGCTGATGAGCAATGAGACTCTGAGGATTCCTGTTCTGTACATTAATAACAC 224
Qy 61 GlnleuCyileuysgluValpHeGlnGlyleAspHrleuysaanglnthAlHis 80
Db 225 CAATGTCGACTGAGAAATCTTTCAGGAAATAGCCACATCGAGAGCTCAAACTGTGCA 284
Qy 81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerleuileuysgluHsileGluArg 100
Db 285 GGGGGTACTGTGGAAGACTATTCAAAAACCTTGTCTTAATAAAGAAATCATTGACGGC 344
Qy 101 GlnLysLysArgCyAlaGlyGluArgTTPArgValThrLysPheLeuAspTYrLeuGln 120
Db 345 CAAAAAAGAAAGTGTGAGAAAGAAAGACGAGAGCTAAACCAATTCCTAGACTACTGCA 404
Qy 121 ValPheLeuGlyValIleAsnThrGluThrProGluSer 134
Db 405 GAGTTCTTGTTGTAATGAACACCGAGTGTAAATAGAAAGT 446

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## RESULT 15

ADG33104  
ID ADG33104 standard; DNA, 816 BP.

AC ADG33104;

DT 26-FEB-2004 (first entry)

DE Human DNA differentially expressed in patients with SLE Segid428.

XX human; de; autoimmune; chronic inflammatory disease; SLE;  
XX systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;  
XX Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;

KW ulcerative colitis; primary sclerosing cholangitis; appendicitis;  
KW diverticulitis; primary biliary sclerosis.

XX Homo sapiens.

PN W02003090694-A2.

XX 06-NOV-2003.

XX 24-APR-2003; 2003WO-US013015.

XX 24-APR-2002; 2002US-00131827.

XX (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX Wohlgemuth J, Fry K, Woodward R, Ly N;

XX WPI; 2003-877243/81.

XX Diagnosing or monitoring autoimmune and chronic inflammatory diseases,  
PT such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative  
PT colitis, psoriasis and asthma by detecting the expression level of one or  
PT more genes.

PS Claim 18; SEQ ID NO 426; 877pp; English.

XX This invention relates to novel methods for diagnosing and monitoring  
CC autoimmune and chronic inflammatory diseases. Specifically, it refers to  
CC the identification of genes that have a clinical utility as diagnostic  
CC tools for the management of, in particular, patients with systemic lupus  
CC erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the  
CC present invention describes a method for determining the levels of  
CC multiple differentially expressed genes of a patient, in a concerted  
CC manner, in order to achieve an improved diagnostic assay with sensitivity  
CC and specificity for the disease in question. As such, these genes are  
CC useful for the diagnosis of various other inflammatory disorders  
CC including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,  
CC ankylosing spondylitis, ulcerative colitis, primary sclerosing  
CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.  
CC This polynucleotide is a DNA sequence representing human mRNA that is  
CC differentially expressed in patients with SLE, used in an exemplification  
CC of the invention.

XX Sequence 816 BP; 276 A; 137 C; 165 G; 238 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.: 1.23e-44 Length: 816  
Score: 430.00 Matches: 87  
Percent Similarity: 77.61% Conservative: 17  
Best Local Similarity: 64.93% Mismatches: 30  
Query Match: 61.78% Indels: 0  
DB: 10 Gaps: 0

US-10-787-382-5 (1-134) x ADG33104 (1-816)

QY 1 MetatgmetleuAanleuSerleuAlaLeuGlyAlaAlaTyrrValSerlaPhe 20  
DB 45 ATGAGGATGCTTGCATTTGAGTTGCTGAGCTTGAGCGCTTACGTATGCGCATC 104  
QY 21 AlavaAlGluAanProMetAanArgleuValAlaGluThrleuThrleuSerThris 40  
DB 105 CCCACAGAAATTCACCAAGATGATGTTGGTGAAGAGACTTGCGACTGCTTTTACTCAT 164  
QY 41 ArgThrTPleuileGlyAspGlyAanleuWetileProthrProGluAanlysaAnhis 60  
DB 165 CGAAGCTGTGATGATGCAATGAGACTCTGAGGATTCCTGTTCCGTACATTAATCAC 224  
QY 61 GluleuCytleuGluValPheGlnGlylleaPThrleuLyAanGlnThrAlahis 80  
DB 225 CAAGCTGCATGCAAGAAATCTTTCAGGAAATGACACCTGAGAGATCAAACTGTGCA 284  
QY 81 GlyGluAlaValAspLyLeuPheGlnAanleuSerleuileGlyHisileGluArg 100

DB 285 GGGGGTACTGTGGAAGACTATTCAAAACTGTCTTAATTAAGAAATACATTGACGGC 344  
QY 101 GlnlyleYsArgCyalaGlyGluArgTrpArgValThrlySPheluAapTyrleuGln 120  
DB 345 CAAAAAAGAGTGTGAGAAAGACGAGAGTAAACCAATTCCTAGACTTACCTGCA 404  
QY 121 ValPheleuGlyValIleAenthrGluTrpThrProGluSer 134  
DB 405 GAGTTCTGTGTATGATGAACCCGAGTGGATTAATAGAAAGT 446

Search completed: August 6, 2005, 21:26:45  
Job time : 375.482 secs

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## OM protein - protein search, using sw model

Run on: August 4, 2005, 17:11:16 ; Search time 114.088 Seconds  
(without alignments)  
458.533 Million cell updates/sec

Title: US-10-787-382-5  
Perfect score: 696  
Sequence: 1 MRMLNLISLALGAAVYSAF.....FLDYLGVLGVINTWTPES 134

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 1752860

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA:\*  
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3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
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5: /cgn2\_6/ptodata/1/pubppaa/PCTUS\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	696	100.0	134	9	US-09-755-633-5
2	696	100.0	134	14	US-10-218-654-81
3	696	100.0	134	14	US-10-262-439-81
4	696	100.0	134	16	US-10-787-382-5
5	610	87.6	115	9	US-09-755-633-10
6	610	87.6	115	14	US-10-218-654-86
7	610	87.6	115	14	US-10-262-439-86
8	610	87.6	115	16	US-10-787-382-10
9	430	61.8	134	14	US-10-289-454-233
10	430	61.8	134	14	US-10-400-377-12
11	430	61.8	134	14	US-10-400-708-12

12	430	61.8	134	14	US-10-298-148-12	Sequence 12, Appl
13	430	61.8	134	14	US-10-050-902-233	Sequence 233, App
14	430	61.8	134	14	US-10-050-898-233	Sequence 233, App
15	430	61.8	134	16	US-10-773-939-12	Sequence 12, Appl
16	430	61.8	134	16	US-10-774-149-12	Sequence 12, Appl
17	430	61.8	134	16	US-10-773-654-12	Sequence 12, Appl
18	430	61.8	134	16	US-10-866-540-12	Sequence 12, Appl
19	430	61.8	134	16	US-10-856-219-12	Sequence 12, Appl
20	430	61.8	134	17	US-10-685-288-12	Sequence 12, Appl
21	430	61.8	134	17	US-10-866-580-12	Sequence 12, Appl
22	430	61.8	134	17	US-10-773-530-12	Sequence 12, Appl
23	430	61.8	134	18	US-10-880-101A-86	Sequence 86, Appl
24	430	61.8	134	18	US-10-880-101A-88	Sequence 86, Appl
25	430	61.8	134	18	US-10-880-101A-90	Sequence 90, Appl
26	430	61.8	134	18	US-10-880-101A-92	Sequence 90, Appl
27	430	61.8	285	14	US-10-295-074-9	Sequence 9, Appl
28	430	61.8	285	14	US-10-295-074-11	Sequence 11, Appl
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31	415.5	59.7	287	14	US-10-295-074-15	Sequence 15, Appl
32	415.5	59.7	287	16	US-10-295-074-13	Sequence 15, Appl
33	413.5	59.4	287	14	US-10-846-911-13	Sequence 13, Appl
34	413.5	59.4	287	16	US-10-846-911-11	Sequence 13, Appl
35	359	51.6	136	14	US-10-289-454-336	Sequence 336, App
36	359	51.6	136	14	US-10-050-902-336	Sequence 336, App
37	359	51.6	136	14	US-10-050-899-336	Sequence 336, App
38	358	51.4	115	16	US-10-658-834A-588	Sequence 588, App
39	357	51.3	115	16	US-10-658-834A-569	Sequence 569, App
40	357	51.3	123	14	US-10-289-454-337	Sequence 337, App
41	357	51.3	123	14	US-10-050-902-337	Sequence 337, App
42	357	51.3	123	14	US-10-050-899-337	Sequence 337, App
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45	357	51.3	115	14	US-10-289-454-234	Sequence 234, App
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47	356	51.1	115	14	US-10-050-899-234	Sequence 234, App
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51	356	51.1	115	16	US-10-658-834A-574	Sequence 574, App
52	356	51.1	115	16	US-10-658-834A-580	Sequence 580, App
53	356	51.1	115	16	US-10-658-834A-587	Sequence 587, App
54	356	51.1	115	16	US-10-658-834A-589	Sequence 589, App
55	356	51.1	115	16	US-10-658-834A-595	Sequence 595, App
56	356	51.1	115	17	US-10-846-911-1	Sequence 1, Appl
57	356	51.1	115	17	US-10-872-199-133	Sequence 133, App
58	355	51.0	115	16	US-10-658-834A-568	Sequence 568, App
59	355	51.0	115	16	US-10-658-834A-575	Sequence 575, App
60	355	51.0	115	16	US-10-658-834A-581	Sequence 581, App
61	355	51.0	115	16	US-10-658-834A-585	Sequence 585, App
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68	353	50.7	115	16	US-10-658-834A-590	Sequence 590, App
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71	352	50.6	115	16	US-10-658-834A-583	Sequence 583, App
72	352	50.6	115	16	US-10-658-834A-594	Sequence 594, App
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85 347 49.9 134 14 US-10-050-902-333 Sequence 333, App  
86 347 49.9 134 14 US-10-050-898-333 Sequence 333, App  
87 344 49.4 136 14 US-10-289-454-332 Sequence 332, App  
88 344 49.4 136 14 US-10-050-902-332 Sequence 332, App  
89 344 49.4 136 14 US-10-050-898-332 Sequence 332, App  
90 343 49.3 133 14 US-10-289-454-235 Sequence 235, App  
91 343 49.3 133 14 US-10-050-902-235 Sequence 235, App  
92 343 49.3 133 14 US-10-050-898-235 Sequence 235, App  
93 343 49.3 133 14 US-10-658-834A-602 Sequence 602, App  
94 343 49.3 131 14 US-10-289-454-334 Sequence 334, App  
95 343 49.3 131 14 US-10-050-902-334 Sequence 334, App  
96 343 49.3 131 14 US-10-050-898-334 Sequence 334, App  
97 342 49.1 115 16 US-10-658-834A-601 Sequence 601, App  
98 76.5 11.0 290 16 US-10-739-930-10556 Sequence 10556, A  
99 75.5 10.8 367 15 US-10-264-237-2786 Sequence 2786, A  
100 75.5 10.8 490 18 US-10-467-535-8 Sequence 8, Appl

## ALIGNMENTS

RESULT 1  
US-09-755-633-5  
Sequence 5, Application US/09755633  
Patent No. US2002012720A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Shumin  
APPLICANT: McCall, Catherine A.  
APPLICANT: Weber, Eric R.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C1-C1  
CURRENT APPLICATION NUMBER: US/09/755,633  
CURRENT FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 5  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-09-755-633-5

Query Match 100.0%; Score 696; DB 9; Length 134;

Best Local Similarity 100.0%; Pred. No. 1,4e-71; Indels 0; Gaps 0;  
Matches 134; Conservative 0; Mismatches 0;

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QY 61 QLCIKVFOGIDITLKNQTAHGAVDKLFONLSIKHIEROKRCAGERRVTKFLDYIQ 120  
DB 61 QLCIKVFOGIDITLKNQTAHGAVDKLFONLSIKHIEROKRCAGERRVTKFLDYIQ 120  
QY 121 VFGLVINTSWTPES 134  
DB 121 VFGLVINTSWTPES 134

RESULT 2  
US-10-218-654-81

Sequence 81, Application US/10218654  
GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Dreletz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C1  
CURRENT APPLICATION NUMBER: US/10/218,654  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: US/09/322,409  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 81  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-10-218-654-81

Query Match 100.0%; Score 696; DB 14; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1,4e-71; Indels 0; Gaps 0;  
Matches 134; Conservative 0; Mismatches 0;

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DB 121 VFGLVINTSWTPES 134

RESULT 3  
US-10-262-439-81

Sequence 81, Application US/10262439  
Publication No. US20030143196A1  
GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Dreletz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/10/262,439  
CURRENT FILING DATE: 2002-09-30  
PRIOR APPLICATION NUMBER: US/09/451,527  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 81  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-10-262-439-81

Query Match 100.0%; Score 696; DB 14; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1,4e-71; Indels 0; Gaps 0;  
Matches 134; Conservative 0; Mismatches 0;

QY 1 MRMLNTSLALGAAYVSAFAVENPMNRLVAETLTLLSTRTWLIGDGLMPTPENKH 60  
DB 1 MRMLNTSLALGAAYVSAFAVENPMNRLVAETLTLLSTRTWLIGDGLMPTPENKH 60  
QY 61 QLCIKVFOGIDITLKNQTAHGAVDKLFONLSIKHIEROKRCAGERRVTKFLDYIQ 120  
DB 61 QLCIKVFOGIDITLKNQTAHGAVDKLFONLSIKHIEROKRCAGERRVTKFLDYIQ 120

Qy	121	VFLGVINTEWTPES	134
Db	121	VFLGVINTEWTPES	134

RESULT 4  
IIS-10-78

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Sequence 5 Application US/10787382
Publication No. US20040191868A1
GENERAL INFORMATION:
APPLICANT: Yang, Shumin
APPLICANT: McCall, Catherine A.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC ACIDS, AND USES THEREOF
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-CI-C1
CURRENT APPLICATION NUMBER: US/10/787,382
CURRENT FILING DATE: 2004-02-24
PRIOR APPLICATION NUMBER: US/09/755,633
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 134
TYPE: PRT
ORGANISM: Canis familiaris
US-10-787-382-5

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Query Match	100.0%	Score 696	DB 16	Length 134
Best Local Similarity	100.0%	Pred. No. 1.4e-71		
Matches 134	Conservative 0	Mismatches 0	Indels 0	Gaps 0

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Db		61 QLCIKEVFQSIDTLKNQTAFHBAVDKLFQNLSLKEHERÖKKRCAGSRWRVTTFELDYIQ 120

Qy	121	VFLGVINTEWTPES	134
Db	121	VFLGVINTEWTPES	134

**RESULT 5**  
**ITS-09-75**

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: Sequence 1: Application US/09755633
: Patent No. US2002127200A1
: GENERAL INFORMATION:
: APPLICANT: Yang, Shumin
: APPLICANT: McCall, Catherine A.
: APPLICANT: Weber, Eric R.
: TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
: FILE REFERENCE: IM-2-C1-C1
: CURRENT APPLICATION NUMBER: US/09/755,633
: CURRENT FILING DATE: 2001-01-05
: PRIOR APPLICATION NUMBER: 09/332,409
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/087,306
: PRIOR FILING DATE: 1998-05-29
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 10
: LENGTH: 115
: TYPE: prt
: ORGANISM: Canis familiaris
: US-09-755-633-10

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Query Match	87.64%	Score	610	DB	9	Length	115
Best Local Similarity	100.0%	Pred. No.	8.3e-62				
Matches	115	Conservative	0	Mismatches	0	Indels	0
						Gaps	0

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Db 1 FAVENPMNRLVAETLTLLSTHRTWLLGDGNLIMPTPENKNHQLCKEVPQSIDTLKNOTA 60

**Dy** 80 HGEAVDKLFQNLISKHEIERQKKR CAGERKRVTKFLDYLVQVPGVINTENTPES 134  
**Db** 61 HGEAVDKLFQNLISKHEIERQKKR CAGERKRVTKFLDYLVQVPGVINTENTPES 115

RESULT 6  
MS-10-21

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Sequence 86, Application US/10218654
Publication No. US2003009609A1
GENERAL INFORMATION:
APPLICANT: Sam, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Drelitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/10/218,654
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 86
LENGTH: 115
TYPE: PR1
ORGANISM: Canis familiaris
US-10-218-654-86

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Query Match	87.6%	Score 610	DB 14	Length 115
Best Local Similarity	100.0%	Pred. No. 8	3e-62	
Matches 115	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy 20 FAVENPMNRLVAETLTLLSTHRTWLTGNGNLMPTPENKQHQLCKEVPFGIDTLNKQTA 79

Db 1 FAVENPMNRLVAETLTLLSTHRTWLTGNGNLMPTPENKQHQLCKEVPFGIDTLNKQTA 66

QY 80 HGEAVDTLPQNLSLKEHIERQKRCAGERNWTKFLDYLVQVFLGVINTEWTPES 134  
DB 61 HGEAVDTLPQNLSLKEHIERQKRCAGERNWTKFLDYLVQVFLGVINTEWTPES 115

RESULT 7  
TIS-10-26

Sequence 86, Application US/10262439  
Publication No. US20030143196A1  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shunlin  
APPLICANT: Dreitz, Matthew J.  
APPLICANT: Wondolilling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/10/262,439  
CURRENT FILING DATE: 2002-09-30  
PRIOR APPLICATION NUMBER: US/09/451,527  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 86  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-10-262-439-86

Query Match 87.6%; Score 610; DB 14; Length 115;  
Best Local Similarity 100.0%; Pred. No. 8.3e-62;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FAVENPMNRLVATLTLLSTHRTWLTGDNLMPTPENKHOCTKEVFGIDTLKNQTA 79  
DB 1 FAVENPMNRLVATLTLLSTHRTWLTGDNLMPTPENKHOCTKEVFGIDTLKNQTA 60

QY 80 HGEAVDKLFGNLSLKEHIEROKKRCGGERWRVTKEFLDYQVFLGVINTEMTES 134  
DB 61 HGEAVDKLFGNLSLKEHIEROKKRCGGERWRVTKEFLDYQVFLGVINTEMTES 115

RESULT 8  
US-10-787-382-10  
Sequence 10, Application US/10787382  
Publication No. US20040191868A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Shumin  
APPLICANT: McCall, Catherine A.  
APPLICANT: Weber, Eric R.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C1-C1  
CURRENT APPLICATION NUMBER: US/10/787,382  
PRIOR FILING DATE: 2004-02-24  
PRIOR APPLICATION NUMBER: US/09/755,633  
PRIOR FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 10  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-10-787-382-10

Query Match 87.6%; Score 610; DB 16; Length 115;  
Best Local Similarity 100.0%; Pred. No. 8.3e-62;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FAVENPMNRLVATLTLLSTHRTWLTGDNLMPTPENKHOCTKEVFGIDTLKNQTA 79  
DB 1 FAVENPMNRLVATLTLLSTHRTWLTGDNLMPTPENKHOCTKEVFGIDTLKNQTA 60

QY 80 HGEAVDKLFGNLSLKEHIEROKKRCGGERWRVTKEFLDYQVFLGVINTEMTES 134  
DB 61 HGEAVDKLFGNLSLKEHIEROKKRCGGERWRVTKEFLDYQVFLGVINTEMTES 115

RESULT 9  
US-10-289-454-233  
Sequence 233, Application US/10289454  
Publication No. US20030157479A1  
GENERAL INFORMATION:  
APPLICANT: Bachmann, Martin  
APPLICANT: Jennings, Gary  
APPLICANT: Sondergeger, Ivo  
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases  
FILE REFERENCE: 1700.0360001  
CURRENT APPLICATION NUMBER: US/10/289,454  
CURRENT FILING DATE: 2003-02-10

PRIOR APPLICATION NUMBER: US 60/396,636  
PRIOR FILING DATE: 2002-07-19  
PRIOR APPLICATION NUMBER: PCT/IB02/00166  
PRIOR FILING DATE: 2002-01-21  
PRIOR APPLICATION NUMBER: US 10/050,902  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: US 60/331,045  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 386  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO: 233  
LENGTH: 134  
TYPE: PRT  
ORGANISM: precursor human IL-5  
US-10-289-454-233

Query Match 61.8%; Score 430; DB 14; Length 134;  
Best Local Similarity 64.9%; Pred. No. 4.8e-41;  
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSTLALGAAYVSAFAVENPMNRLVATLTLLSTHRTWLTGDNLMPTPENKHO 60  
DB 1 MRMLNLSTLALGAAYVAIPTEIPTSALVKETLALSTHRTLLINERTLRIPVPHKOH 60

QY 61 QLCIKVFGIDTLKNQTAHGEAVDKLFGNLSLKEHIEROKKRCGGERWRVTKEFLDYQ 120  
DB 61 QLCIKVFGIDTLKNQTAHGEAVDKLFGNLSLKEHIEROKKRCGGERWRVTKEFLDYQ 120

QY 121 VFLGVINTEMTES 134  
DB 121 EFLGVINTEMTES 134

RESULT 10  
US-10-400-377-12  
Sequence 12, Application US/10400377  
Publication No. US20030162949A1  
GENERAL INFORMATION:  
APPLICANT: Cox III, George N  
APPLICANT: Bolder Biotechnology, Inc.  
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins  
FILE REFERENCE: 4152-1-PUS  
CURRENT APPLICATION NUMBER: US/10/400,377  
PRIOR FILING DATE: 2003-03-26  
PRIOR APPLICATION NUMBER: US/09/462,941  
PRIOR FILING DATE: 2000-01-14  
PRIOR APPLICATION NUMBER: 60/052,516  
PRIOR FILING DATE: 1997-07-14  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 12  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-400-377-12

Query Match 61.8%; Score 430; DB 14; Length 134;  
Best Local Similarity 64.9%; Pred. No. 4.8e-41;  
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSTLALGAAYVSAFAVENPMNRLVATLTLLSTHRTWLTGDNLMPTPENKHO 60  
DB 1 MRMLNLSTLALGAAYVAIPTEIPTSALVKETLALSTHRTLLINERTLRIPVPHKOH 60

QY 61 QLCIKVFGIDTLKNQTAHGEAVDKLFGNLSLKEHIEROKKRCGGERWRVTKEFLDYQ 120  
DB 61 QLCIKVFGIDTLKNQTAHGEAVDKLFGNLSLKEHIEROKKRCGGERWRVTKEFLDYQ 120

QY 121 VFLGVINTEMTES 134  
DB 121 EFLGVINTEMTES 134





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 4, 2005, 16:50:05 ; Search time 134.538 Seconds  
(without alignments)  
385.213 Million cell updates/sec

Title: US-10-787-382-5  
Perfect score: 696  
Sequence: 1 MRLMLNLILALGAAYVSAR.....FLDYLVGVLCVINTWTPES 134

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseq1980s:\*  
2: geneseq1990s:\*  
3: geneseq2000s:\*  
4: geneseq2001s:\*  
5: geneseq2002s:\*  
6: geneseq2003as:\*  
7: geneseq2003bs:\*  
8: geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	100.0	134	3	AAV58219 Canine in
2	687	98.7	134	4	AAV72615 Canine in
3	610	87.6	115	3	AAV58220 Canine ma
4	536	77.0	132	2	AAW08479 Ovine IL-
5	430	61.8	134	2	AAV92802 Human int
6	430	61.8	134	4	AAV72617 Human int
7	430	61.8	134	5	ABG94294 Human int
8	430	61.8	134	5	ABG94294 Human int
9	430	61.8	134	5	ABG94294 Human int
10	430	61.8	134	5	ABG94294 Human int
11	430	61.8	134	7	ADP70849 Human int
12	430	61.8	134	8	ADP56010 Human int
13	430	61.8	285	6	AAO30457 Human PRO
14	430	61.8	285	6	AAO30457 Human PRO
15	429	61.6	84	4	AAV72616 Canine in
16	426	61.2	134	5	AAU10354 Interleuk
17	420	60.3	287	6	AAO30460 hirs.37 v
18	415.5	59.7	287	6	AAO30460 hirs.37 v
19	413.5	59.4	287	6	AAO30460 hirs.36 v
20	376	54.0	133	2	AAV7064 Murine ec
21	376	54.0	133	2	AAV96963 T cell re
22	376	54.0	133	2	AAV72949 T cell re
23	376	54.0	133	2	AAV72947 T cell re
24	376	54.0	133	4	AAV72618 Murine in
25	375	53.9	133	1	AAV82969 B cell di

26	359	51.6	136	5	ABG94352 Human C-I
27	359	51.6	136	5	ABG80664 Human ILn
28	359	51.6	136	7	ADK17223 Human C-I
29	358	51.4	115	8	ADL89254 Human mod
30	357	51.3	113	1	AAV93152 Sequence
31	357	51.3	115	8	ADL89235 Human mod
32	357	51.3	123	5	ABG94353 Human C-I
33	357	51.3	123	5	ABG80665 Human IL-
34	357	51.3	123	7	ADK17224 Human C-I
35	357	51.3	138	5	ABG94351 Human C-I
36	357	51.3	138	5	ABG80663 Human ILn
37	357	51.3	138	7	ADK17222 Human C-I
38	356	51.1	112	1	AAV80279 Plectrop
39	356	51.1	115	1	AAV81038 Sequence
40	356	51.1	115	3	AAV84589 Human int
41	356	51.1	115	5	ABG94295 Human mat
42	356	51.1	115	5	ABG80607 Human mat
43	356	51.1	115	6	AAO30453 Human mat
44	356	51.1	115	7	ADK17208 Human int
45	356	51.1	115	8	ADL89253 Human mod
46	356	51.1	115	8	ADL89251 Human mod
47	356	51.1	115	8	ADL89247 Human mod
48	356	51.1	115	8	ADL89240 Human mod
49	356	51.1	115	8	ADL89246 Human mod
50	356	51.1	115	8	ADL89255 Human mod
51	355	51.0	115	8	ADL89251 Human mod
52	355	51.0	115	8	ADL89252 Human mod
53	355	51.0	115	8	ADL89247 Human mod
54	355	51.0	115	8	ADL89241 Human mod
55	355	51.0	115	8	ADL89234 Human mod
56	355	51.0	115	8	ADL89263 Human mod
57	355	51.0	133	1	AAV80280 Murine pl
58	354	50.9	115	8	ADL89248 Human mod
59	354	50.9	115	8	ADL89252 Human mod
60	354	50.9	115	8	ADL89242 Human mod
61	353	50.7	115	8	ADL89243 Human mod
62	353	50.7	115	8	ADL89256 Human mod
63	353	50.7	115	8	ADL89264 Human mod
64	352	50.6	115	8	ADL89260 Human mod
65	352	50.6	115	8	ADL89249 Human mod
66	352	50.6	115	8	ADL89238 Human mod
67	351	50.4	115	8	ADL89239 Human mod
68	351	50.4	115	8	ADL89250 Human mod
69	351	50.4	115	8	ADL89259 Human mod
70	351	50.4	115	8	ADL89245 Human mod
71	351	50.4	115	8	ADL89244 Human mod
72	351	50.4	115	8	ADL89258 Human mod
73	351	50.4	115	8	ADL89265 Human mod
74	351	50.4	115	8	ADL89257 Human mod
75	351	50.4	115	2	AAV43436 Human int
76	351	50.4	115	8	ADL89236 Human mod
77	348	50.0	115	8	ADL89237 Human mod
78	347	49.9	115	2	AAV05273 N-termina
79	347	49.9	115	2	AAV72948 Truncated
80	347	49.9	115	5	ABG94349 Mouse C-I
81	347	49.9	134	5	ABG80661 Mouse IL-
82	347	49.9	134	7	ADK17220 Mouse C-I
83	347	49.9	136	5	ABG94348 Mouse C-I
84	344	49.4	136	7	ADK17209 Mouse int
85	344	49.4	136	7	ADK17219 Mouse C-I
86	344	49.4	136	7	ADK17219 Mouse C-I
87	343	49.3	113	2	AAV05274 N-termina
88	343	49.3	113	5	ABG94266 Mouse int
89	343	49.3	113	5	ABG80608 Mouse mat
90	343	49.3	113	7	ADK17209 Mouse int
91	343	49.3	115	8	ADL89268 Human mod
92	343	49.3	121	5	ABG94350 Mouse C-I
93	343	49.3	121	5	ABG80662 Mouse IL-
94	343	49.3	121	7	ADK17221 Mouse C-I
95	342	49.1	112	2	AAV05275 N-termina
96	342	49.1	115	8	ADL89267 Human mod
97	339	48.7	126	3	AAV84594 Modified
98	335	48.1	132	3	AAV84598 Modified

99 332.5 47.8 126 3 AAB45490 Aab45490 Modified  
100 332.5 47.8 126 3 AAB45514 Aab45514 Modified

## ALIGNMENTS

RESULT 1  
ID AAY58219 standard; protein; 134 AA.  
XX  
AC AAY58219;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-5 (IL-5).  
XX  
KM Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
XX  
OS Canis familiaris.  
XX  
PN MO961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99MO-US011942.  
XX  
PR 29-MAY-1998; 98US-0087306P.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dretz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
XX  
N-PSDB; AAZ55546, AAZ55547, AAZ55548, AAZ55549.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
XX  
PS useful for treating or preventing e.g. tumours or autoimmune disease.  
XX  
PS Claim 3b; Page 224; 264pp; English.  
XX  
CC Sequence AAY58219-Y58220 represent encoded and mature canine interleukin  
CC -5 (IL-5). The invention relates to canine IL-4, canine or feline Flt-3  
CC ligand, canine or feline CD40, canine or feline CD134 (CD40 ligand),  
CC canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline  
CC granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides  
CC which encode these immunoregulatory proteins. The proteins, their  
CC associated nucleic acids, specific antibodies and inhibitors may be used  
CC as vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans). They  
CC may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase the  
CC response from a co-administered antigen. The nucleotide sequences can  
CC also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for modulators  
CC of activity, while the antibodies may be used in detection, and in drug  
CC targeting  
XX  
SQ Sequence 134 AA;

Query Match 100.0%; Score 696; DB 3; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1e-74;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRMLNLSLALGAAYVSAFAVENPMNRVAETLTLSHRTWLGDNLMPTPENKH 60  
DB 1 MRMLNLSLALGAAYVSAFAVENPMNRVAETLTLSHRTWLGDNLMPTPENKH 60  
QY 61 QLCIKVFGQIDITLNQTAHGAVDKLFONLSLKEHIEROKRCAGRRRVTKFLDYIQ 120  
DT

DB 61 QLCIKVFGQIDITLNQTAHGAVDKLFONLSLKEHIEROKRCAGRRRVTKFLDYIQ 120  
QY 121 VFLGVINTWTPES 134  
DB 121 VFLGVINTWTPES 134

RESULT 2  
ID AAB72615 standard; protein; 134 AA.  
XX  
AC AAB72615;  
XX  
DT 04-MAY-2001 (first entry)  
XX  
DE Canine interleukin-5 protein #1.  
XX  
KM Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;  
KW Inflammatory reaction.  
XX  
OS Canis sp.  
XX  
PN MO200111049-A2.  
XX  
PD 15-FEB-2001.  
XX  
PF 09-AUG-2000; 2000MO-US021651.  
XX  
PR 10-AUG-1999; 99US-00371615.  
XX  
PA (IDEX-) IDEXX LAB INC.  
XX  
PI Quo H, Lawton R, Mermer B, Aiyappa AP;  
XX  
DR WPI; 2001-191542/19.  
XX  
N-PSDB; AAF74300.  
XX  
PT Novel canine interleukin 5 polynucleotide and polypeptides are used for  
XX  
PS generating antibodies which are useful in treating allergies in dogs.  
XX  
PS Claim 29; Page 46-47; 48pp; English.  
XX  
CC The present invention provides the protein and coding sequences of the  
CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,  
CC cancer and inflammatory reactions in dogs. The present sequence is one  
CC version of the IL-5 protein shown in the specification  
XX  
SQ Sequence 134 AA;

Query Match 98.7%; Score 687; DB 4; Length 134;  
Best Local Similarity 99.3%; Pred. No. 1.2e-73;  
Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRMLNLSLALGAAYVSAFAVENPMNRVAETLTLSHRTWLGDNLMPTPENKH 60  
DB 1 MRMLNLSLALGAAYVSAFAVENPMNRVAETLTLSHRTWLGDNLMPTPENKH 60  
QY 61 QLCIKVFGQIDITLNQTAHGAVDKLFONLSLKEHIEROKRCAGRRRVTKFLDYIQ 120  
DB 61 QLCIKVFGQIDITLNQTAHGAVDKLFONLSLKEHIEROKRCAGRRRVTKFLDYIQ 120  
QY 121 VFLGVINTWTPES 134  
DB 121 VFLGVINTWTPES 134  
RESULT 3  
ID AAY58220 standard; protein; 115 AA.  
XX  
AC AAY58220;  
XX  
DT 14-MAR-2000 (first entry)





XX 24-MAY-1996 (first entry)  
DT Human interleukin-5.  
XX  
XX Cytokine; interleukin-5; agonist; antagonist; diagnosis; therapy;  
XX cancer; inflammation; degenerative disease.  
XX  
XX Homo sapiens.  
XX MO9604306-A2.  
XX  
XX 15-FEB-1996.  
XX  
XX 31-JUL-1995; 95WO-US008950.  
XX  
XX 01-AUG-1994; 94US-00284393.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Zurawski SM, Zurawski G;  
XX  
XX WPI; 1996-129335/13.  
XX  
XX Mut(e)n(s) of human and murine cytokine(s), esp. interleukin(s) and murine  
PT P600 contg. amino acid substitutions. - useful for the diagnosis and  
PT treatment of cancer, inflammation, etc.  
XX  
XX Disclosure; Page 43; 52pp; English.  
XX  
XX Mut(e)n(s) of human interleukin-5 (AAR92802) and other cytokines (see also  
CC AAR92790-801) are obt'd. by site-directed mutagenesis of natural cytokine  
CC sequences at positions identified as critical for activity. The mut(e)n  
CC are useful in the screening of cytokine and cytokine receptor levels, and  
CC in the diagnosis or treatment of e.g. inflammation, cancer, and  
CC degenerative disorders  
XX  
XX Sequence 134 AA;  
SQ

Query Match 61.8%; Score 430; DB 2; Length 134;  
Best Local Similarity 64.9%; Pred. No. 6.8e-43;  
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSTLALGAAYVSAFAVENPMNRVLAETLTLLSTRTWLIGDGNLMIPTPENKNH 60  
DB 1 MRMLNLSTLALGAAYVVAIPTEIPTSALVKETLALSTRITLLINERTLRIPVPHKNH 60  
QY 61 QLCIKVEFGIDITLKNQTAHGEAVDKLFONTSLIKHIEROKKRCAGERRVTKFLDYIQ 120  
DB 61 QLCIEBIFOGIGTLESQTVQGTVGRVLFKNLSLKKYIDGQKKKCGERRRVNOFLDYIQ 120  
QY 121 VFLGVINTEWTPES 134  
DB 121 EFLGVNTEWITIS 134

RESULT 6  
AAB72617  
ID AAB72617 standard; protein; 134 AA.  
XX  
XX AAB72617;  
XX  
XX 04-MAY-2001 (first entry)  
XX  
XX Human interleukin-5.  
XX  
XX Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;  
XX inflammatory reaction; human.  
XX  
XX Homo sapiens.  
XX  
XX MO200111049-A2.  
XX

PD 15-FEB-2001.  
XX  
XX 09-AUG-2000; 2000WO-US021651.  
XX  
XX 10-AUG-1999; 99US-00371615.  
XX  
XX (IDEXX ) IDEXX LAB INC.  
XX  
XX Guo H, Lawton R, Warner B, Aiyappa AP;  
XX  
XX WPI; 2001-191542/19.  
XX  
XX Novel canine interleukin 5 polynucleotide and polypeptides are used for  
PT generating antibodies which are useful in treating allergies in dogs.  
XX  
XX Disclosure; Fig 2; 48pp; English.  
XX  
XX The present invention provides the protein and coding sequences of the  
CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,  
CC cancer and inflammatory reactions in dogs. The present sequence is human  
CC IL-5  
XX  
XX Sequence 134 AA;  
SQ

Query Match 61.8%; Score 430; DB 4; Length 134;  
Best Local Similarity 64.9%; Pred. No. 6.8e-43;  
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSTLALGAAYVSAFAVENPMNRVLAETLTLLSTRTWLIGDGNLMIPTPENKNH 60  
DB 1 MRMLNLSTLALGAAYVVAIPTEIPTSALVKETLALSTRITLLINERTLRIPVPHKNH 60  
QY 61 QLCIKVEFGIDITLKNQTAHGEAVDKLFONTSLIKHIEROKKRCAGERRVTKFLDYIQ 120  
DB 61 QLCIEBIFOGIGTLESQTVQGTVGRVLFKNLSLKKYIDGQKKKCGERRRVNOFLDYIQ 120  
QY 121 VFLGVINTEWTPES 134  
DB 121 EFLGVNTEWITIS 134

RESULT 7  
ABG94294  
ID ABG94294 standard; protein; 134 AA.  
XX  
XX ABG94294;  
XX  
XX 10-DEC-2002 (first entry)  
XX  
XX Human interleukin 5 precursor protein.  
XX  
XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;  
XX cytotoxic; antiviral; antidiabetic; hypoglycaemic; antigen array;  
XX vaccine; infectious disease.  
XX  
XX Homo sapiens.  
XX  
XX MO200256905-A2.  
XX  
XX 25-JUL-2002.  
XX  
XX 21-JAN-2002; 2002WO-IB000166.  
XX  
XX 19-JAN-2001; 2001US-0262379P.  
XX  
XX 04-MAY-2001; 2001US-0288549P.  
XX  
XX 05-OCT-2001; 2001US-0326998P.  
XX  
XX 07-NOV-2001; 2001US-0331045P.  
XX  
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.  
XX  
XX Renner WA, Bachmann M, Tilsot A, Maurer P, Lechner F, Sebbel P;  
PI Plosek C;  
XX

DR WPI; 2002-627351/67.

XX Molecular antigen array used in the production of vaccines for infectious  
PT diseases.

XX Disclosure; Page 422; 441pp; English.

XX This invention relates to a novel ordered and repetitive antigen array  
CC used in the production of vaccines for infectious diseases. The invention  
CC also discloses a composition comprising a non-natural molecular scaffold  
CC comprising a core particle selected from a core particle of a non-natural  
CC origin and a core particle of natural origin and an organiser comprising  
CC at least one first attachment site, where the organiser is connected to  
CC the core particle by at least one covalent bond. Also disclosed is an  
CC antigen or antigenic determinant with at least one second attachment  
CC site, where the antigen or antigenic determinant is amyloid beta peptide  
CC (Abeta1-42) or its fragment and where the second attachment site is  
CC selected from an attachment site not naturally occurring with the antigen  
CC or antigenic determinant and an attachment site naturally occurring with  
CC the antigen or antigenic determinant, where the second attachment site is  
CC capable of association through at least one non-peptide bond to the first  
CC attachment site and where the antigen or antigenic determinant and the  
CC scaffold interact through the association to form an ordered and  
CC repetitive antigen array. The invention also comprises a coat protein  
CC capable of forming a capsid which comprises mutant  $\beta$  subunit coat proteins  
CC having an amino acid sequence selected from five amino acid sequences  
CC fully defined in the specification. The compounds of the invention may  
CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,  
CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in  
CC immunisation and as a vaccine. The present sequence represents a protein  
CC sequence used to create the compositions of the invention

XX Sequence 134 AA;

Query Match 61.8%; Score 430; DB 5; Length 134;

Best Local Similarity 64.9%; Pred. No. 6, 8e-43; Mismatches 0; Gaps 0;

Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRRLNLSTLALGAAYVSAFAVENPMNRVLAETLTLLSTHRTWLGNGMLTPPENKN 60

DB 1 MRRLNLSTLALGAAYVSAFAVENPMNRVLAETLTLLSTHRTWLGNGMLTPPENKN 60

QY 61 QLCIKFVPGIDITLKNQTAHGEAVDKLFQNLSTLKEIHIEKRCGGERVWTKFLDYQ 120

DB 61 QLCIKFVPGIDITLKNQTAHGEAVDKLFQNLSTLKEIHIEKRCGGERVWTKFLDYQ 120

QY 121 VPLGVINTEWTPES 134

DB 121 VPLGVINTEWTPES 134

QY 121 EPLGVINTEWTPES 134

DB 121 EPLGVINTEWTPES 134

QY 121 EPLGVINTEWTPES 134

DB 121 EPLGVINTEWTPES 134

QY 121 EPLGVINTEWTPES 134

DB 121 EPLGVINTEWTPES 134

QY 121 EPLGVINTEWTPES 134

DB 121 EPLGVINTEWTPES 134

QY 121 EPLGVINTEWTPES 134

DB 121 EPLGVINTEWTPES 134

QY 121 EPLGVINTEWTPES 134

DB 121 EPLGVINTEWTPES 134

OS Homo sapiens.

XX WO200256907-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-1B000168.

XX 19-JAN-2001; 2001US-0262379P.

XX 04-MAY-2001; 2001US-0288549P.

XX 05-OCT-2001; 2001US-0326998P.

XX 07-NOV-2001; 2001US-0331045P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX (NOVO-) NOVARTIS PHARMA AG.

XX (MAUR-) MAURER P.

XX (LECH-) LECHNER F.

XX (ORTM-) ORTMANN R.

XX (LUEB-) LUEBEND R.

XX (STAU-) STAUFENBIEL M.

XX (FREV-) FREY P.

XX MAURER P., Lechner F., Ortmann R., Luebend R., Staufenbiel M., Frey P.,

XX Renner WA, Bachmann M, Tissot A, Sebbel P, Floseek C,

XX WPI; 2002-636514/68.

XX Molecular antigen array used in the production of vaccines for infectious

XX diseases.

XX Disclosure; Page 399; 418pp; English.

XX The invention relates to a composition comprising: (a) a non-natural

XX molecular scaffold comprising: (i) a core particle selected from: (1) a

XX core particle of a non-natural origin; and (2) a core particle of natural

XX origin; and (ii) an organiser comprising at least one first attachment

XX site, where the organiser is connected to the core particle by at least

XX one covalent bond; (b) an antigen or antigenic determinant with at least

XX one second attachment site, where the antigen or antigenic determinant is

XX amyloid beta peptide (Abeta 1-42) or its fragment, and where the second

XX attachment site is selected from: (i) an attachment site not naturally

XX occurring with the antigen or antigenic determinant; and (ii) an

XX attachment site naturally occurring with the antigen or antigenic

XX determinant, where the second attachment site is capable of association

XX through at least one non-peptide bond to the first attachment site; and

XX where the antigen or antigenic determinant and the scaffold interact

XX through the association to form an ordered and repetitive antigen array.

XX Also included is a process for producing a non-naturally occurring

XX ordered and repetitive antigen array. The composition is used in

XX immunisation and as a vaccine for diseases such as influenza, graft

XX versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult

XX respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,

XX acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,

XX systemic lupus erythematosus, inflammatory immune diseases, myasthenia

XX gravis, immunoproliferative disease lymphadenopathy,

XX angiotensinoproliferative lymphadenopathy, immunoblastic lymphadenopathy,

XX rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,

XX osteoporosis and infectious diseases. The present sequence is an antigen

XX for use in the array of the invention. The antigen is modified to possess

XX a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-

XX or C-terminal linker peptide which serves as the attachment point to a

XX virus like particle or bacterial protein (the scaffold protein)

XX Sequence 134 AA;

Query Match 61.8%; Score 430; DB 5; Length 134;

Best Local Similarity 64.9%; Pred. No. 6, 8e-43;

Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRRLNLSTLALGAAYVSAFAVENPMNRVLAETLTLLSTHRTWLGNGMLTPPENKN 60

DB 1 MRRLNLSTLALGAAYVSAFAVENPMNRVLAETLTLLSTHRTWLGNGMLTPPENKN 60

QY 61 QLCIKFVPGIDITLKNQTAHGEAVDKLFQNLSTLKEIHIEKRCGGERVWTKFLDYQ 120

DB 61 QLCIKFVPGIDITLKNQTAHGEAVDKLFQNLSTLKEIHIEKRCGGERVWTKFLDYQ 120

QY 121 VPLGVINTEWTPES 134

DB 121 VPLGVINTEWTPES 134

QY 121 EPLGVINTEWTPES 134

DB 121 EPLGVINTEWTPES 134

QY 121 EPLGVINTEWTPES 134

DB 121 EPLGVINTEWTPES 134

QY 121 EPLGVINTEWTPES 134

DB 121 EPLGVINTEWTPES 134

QY 121 EPLGVINTEWTPES 134

DB 121 EPLGVINTEWTPES 134

QY 121 EPLGVINTEWTPES 134

DB 121 EPLGVINTEWTPES 134

QY 121 EPLGVINTEWTPES 134

DB 121 EPLGVINTEWTPES 134

QY 121 EPLGVINTEWTPES 134

DB 121 EPLGVINTEWTPES 134

QY 61 QCTCKEYFQIGIDTLKNGTAHGAENVKLFQNLISLKEHIEROKRCAGERNVTKFLDYIQ 120  
 DB 61 QCTCKEYFQIGIDTLKNGTAHGAENVKLFQNLISLKEHIEROKRCAGERNVTKFLDYIQ 120  
 QY 121 VFLLGVNTEWTPES 134  
 DB 121 VFLLGVNTEWTPES 134

## RESULT 9

AAU10353  
 ID AAU10353 standard; protein; 134 AA.

AC AAU10353;  
 DT 14-FEB-2002 (first entry)  
 DE Interleukin 5 (IL5).  
 KW Human; interleukin 5; IL5; antiinflammatory; antiasthmatic; asthma;  
 KM haplotyping; inflammatory disorder.  
 OS Homo sapiens.  
 PN MO200177132-A2.  
 PD 18-OCT-2001.  
 PF 11-APR-2001; 2001MO-US012011.  
 PR 11-APR-2000; 2000US-0196250P.  
 PX (GENA-) GENA15ANCE PHARM INC.  
 PI Bentivegna SC, Chew A, Choi JY, Denton RR, Kazemi A;  
 PI Nandabalan K, Parks KE;  
 DR MPI; 2002-041289/05.  
 DR N-PSDB; AAS15002.

PT New haplotypes of the human interleukin 5 gene, useful to diagnose and  
 PT treat diseases associated with the gene including inflammatory disorders  
 PT such as asthma.  
 PS Claim 27; Fig 3; 65bp; English.

CC The invention relates to haplotyping the human interleukin 5 (IL5) gene  
 CC of an individual, comprising determining if the individual has one of the  
 CC IL5 haplotypes or haplotype pairs fully defined in the specification.  
 CC Haplotyping the IL5 gene of an individual, comprises determining the  
 CC identity of the nucleotide at two or more polymorphic sites in one copy  
 CC of the gene. The method also involves identifying an association between  
 CC a trait and a haplotype or haplotype pair of the IL5 gene, comprising  
 CC comparing the frequency of the haplotype/pair in a population exhibiting  
 CC the trait with that of a reference population. A higher frequency in the  
 CC trait population indicates the trait is associated with the haplotype.  
 CC The polymucleotides and screened compounds are useful to develop  
 CC treatment for diseases associated with IL-5 activity including  
 CC inflammatory disorders such as asthma. The present sequence represents  
 CC the amino acid sequence of interleukin 5 (IL5) as described in the method  
 CC of the invention

CC Sequence 134 AA;

Query Match 61.8%; Score 430; DB 5; Length 134;  
 Best Local Similarity 64.9%; Pred. No. 6.8e-43;  
 Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRRLNLSTLALGAAYVSAFAVENPMRLVAETLLSTHRTWLIGDGNIMPTPENKH 60  
 DB 1 MRRLNLSTLALGAAYVSAFAVENPMRLVAETLLSTHRTWLIGDGNIMPTPENKH 60  
 QY 61 QCTCKEYFQIGIDTLKNGTAHGAENVKLFQNLISLKEHIEROKRCAGERNVTKFLDYIQ 120

DB 61 QCTCKEYFQIGIDTLKNGTAHGAENVKLFQNLISLKEHIEROKRCAGERNVTKFLDYIQ 120  
 QY 121 VFLLGVNTEWTPES 134  
 DB 121 VFLLGVNTEWTPES 134

## RESULT 10

ADF70849  
 ID ADF70849 standard; protein; 134 AA.

AC ADF70849;  
 DT 12-FEB-2004 (first entry)  
 DE Human Interleukin 5 (IL-5).  
 KW Immunostimulant; granulocyte macrophage colony stimulating factor;  
 KM GM-CSF; neutropenia; myelosuppressive chemotherapy;  
 KM bone marrow transplantation; HIV infection; burn; surgery; dilatation;  
 KM anaemia; neonatal septicemia; severe chronic neutropenia;  
 KM aplastic anaemia; acute leukaemia; human; growth hormone super family;  
 KW Interleukin 5; IL-5.  
 OS Homo sapiens.  
 PN US2003171284-A1.  
 PD 11-SEP-2003.  
 PF 15-NOV-2002; 2002US-00298148.  
 PX 14-JUL-1997; 97US-0052516P.  
 PR 13-JUL-1998; 98WO-US014497.  
 PR 14-JAN-2000; 2000US-00462941.  
 PR 15-NOV-2001; 2001US-0332285P.  
 PR 11-OCT-2002; 2002US-0418040P.

PA (COXG/) COX G N.  
 PA (DOHE/) DOHERTY D H.  
 PI Cox GN, Doherty DH;  
 DR MPI; 2003-898295/82.

PT Protecting an animal from a disease or condition, useful for treating  
 PT neutropenia, comprises administering to an animal having the disease or  
 PT condition a composition comprising GM-CSF cysteine mutein.

PS Example 11; SEQ ID NO 12; 56bp; English.

CC The invention describes protecting an animal from a disease or condition  
 CC that can be treated by wild-type granulocyte macrophage colony  
 CC stimulating factor (GM-CSF) comprising administering to an animal having  
 CC the disease or condition a composition comprising GM-CSF cysteine mutein.  
 CC The methods are useful for preventing or treating the occurrence of  
 CC neutropenia in an animal, the neutropenia is selected from neutropenia  
 CC resulting from myelosuppressive chemotherapy, neutropenia associated with  
 CC bone marrow transplantation, neutropenia associated with infection with  
 CC the human immunodeficiency virus, neutropenia associated with burns,  
 CC surgery, dilatation, anaemia and neonatal septicemia, severe chronic  
 CC neutropenia, neutropenia associated with aplastic anaemia and acute  
 CC leukaemia. This is the amino acid sequence of human interleukin 5 (IL-5),  
 CC a member of the growth hormone super family which also includes GM-CSF.

CC Sequence 134 AA;

Query Match 61.8%; Score 430; DB 7; Length 134;  
 Best Local Similarity 64.9%; Pred. No. 6.8e-43;  
 Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRRLNLSTLALGAAYVSAFAVENPMRLVAETLLSTHRTWLIGDGNIMPTPENKH 60

Db 1 MRMLHSLSLALGAAVYVAIPTEIPTSALVKTETLALSTRHTLLIANETLRIPVPAKNH 60  
Qy 61 QLCIKVEFGQIDITLKNQTAGBAVDKLFQNLISLKEHIEROKRCAGERRRVYTFDYLO 120  
Db 61 QLCIEEIFQGIIGLESQTVGGTVGRFLFKNLISLKKYIDQKKCKGERRRVNQFDYLO 120  
Qy 121 VFLGVINTEWTPES 134  
Db 121 EFLGVNTEWTEWIES 134

RESULT 11  
ADK17207  
ID ADK17207 standard; protein; 134 AA.  
AC ADK17207;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human interleukin-5 precursor for repetitive antigen array.  
XX  
KW antiallergic; antiasthmatic; cytostatic; vaccine; virus-like particle;  
KW interleukin; IL-5; IL-13; eosin; repetitive antigen array;  
KW allergic eosinophilic disease; asthma; Hodgkin's lymphoma.  
XX  
OS Homo sapiens.  
XX  
PN WO2003040164-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 07-NOV-2002; 2002WO-EP012455.  
XX  
PR 07-NOV-2001; 2001US-0331045P.  
XX  
PR 18-JAN-2002; 2002US-00050902.  
XX  
PR 21-JAN-2002; 2002WO-1B000166.  
XX  
PR 19-JUL-2002; 2002US-0396636P.  
XX  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
XX  
PI Bachmann M, Jennings G, Sonderegger I;  
XX  
DR WPI; 2003-441518/41.  
XX  
PT Composition comprising an ordered and repetitive antigen or antigenic  
PT determinant array, useful as a medicament, or for manufacturing a  
PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or  
PT Hodgkin's lymphoma.  
XX  
PS Disclosure; SEQ ID NO 233; 245bp; English.  
XX  
CC The invention relates to a composition comprising a virus-like particle  
CC and at least one antigen, which is a protein or peptide of interleukin  
CC (IL)-5, IL-13 or eosin, and is bound to the virus-like particle, or a  
CC core particle with at least one first attachment site and at least one  
CC antigen with at least one second attachment site, where the antigen is a  
CC protein or peptide of IL-5, IL-13 or eosin. The second attachment site  
CC is an attachment site naturally or not naturally occurring with the  
CC antigen or antigenic determinant. The second attachment site is capable  
CC of association to the first attachment site, and where the antigen or  
CC antigenic determinant and the core particle interact through the  
CC association to form an ordered and repetitive antigen array. The  
CC compositions are useful as medicaments, or for manufacturing a medicament  
CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or  
CC Hodgkin's lymphoma and related diseases. This sequence is used to  
CC generate the compound of the invention.  
XX  
SQ Sequence 134 AA;

Query Match 61.8%; Score 430; DB 7; Length 134;  
Best Local Similarity 64.9%; Pred. No. 6.8e-43;  
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MRMLHSLSLALGAAVYVAIPTEIPTSALVKTETLALSTRHTLLIANETLRIPVPAKNH 60  
Db 1 MRMLHSLSLALGAAVYVAIPTEIPTSALVKTETLALSTRHTLLIANETLRIPVPAKNH 60  
Qy 61 QLCIKVEFGQIDITLKNQTAGBAVDKLFQNLISLKEHIEROKRCAGERRRVYTFDYLO 120  
Db 61 QLCIEEIFQGIIGLESQTVGGTVGRFLFKNLISLKKYIDQKKCKGERRRVNQFDYLO 120  
Qy 121 VFLGVINTEWTPES 134  
Db 121 EFLGVNTEWTEWIES 134

RESULT 12  
ADP56010  
ID ADP56010 standard; protein; 134 AA.  
AC ADP56010;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human PRO protein sequence SEQ ID NO:1986.  
XX  
KW human; PRO; immune related disease; inflammatory immune response;  
KW immune response stimulation; antiallergic; antiaesthetic; antiarthritic;  
KW antiaesthetic; antidiabetic; antiinflammatory; antipneumatic;  
KW antineumatic; antichyroid; CNS; dermatological; gastrointestinal;  
KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;  
KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;  
KW virucide; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO2004039956-A2.  
XX  
PD 13-MAY-2004.  
XX  
PF 28-OCT-2003; 2003WO-US034381.  
XX  
PR 29-OCT-2002; 2002US-0422472P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;  
PI Wood WI, Wu TD;  
XX  
DR WPI; 2004-376182/35.  
XX  
PS Claim 1; SEQ ID NO 1986; 3009bp; English.  
XX  
CC The present invention describes an isolated PRO nucleic acid (1). Also  
CC described: (1) a vector comprising (1); (2) a host cell comprising the  
CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an  
CC isolated PRO polypeptide; (5) a chimeric molecule comprising the  
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an  
CC antibody which specifically binds to a polypeptide of (4); (7) a  
CC composition of matter comprising a polypeptide of (4), an agonist or  
CC antagonist of the polypeptide or an antibody that binds to the  
CC polypeptide in combination with a carrier; (8) an article of manufacture  
CC comprising a container, a label on the container and a composition of  
CC matter of (7); (9) a method of treating an immune related disease in a  
CC mammal; (10) a method for determining the presence of a PRO polypeptide  
CC in a sample suspected of having the polypeptide; (11) a method of  
CC diagnosing an immune related disease or an inflammatory immune response  
CC in mammal; (12) a method of identifying a compound that inhibits or  
CC mimics the activity of or expression of a gene encoding a PRO polypeptide

CC ; and (13) a method of stimulating the immune response in a mammal. The  
 CC PRO sequences have antiallergic, antianaemic, antiarthritic,  
 CC antileptemic, antidiabetic, antiinflammatory, antipsoriatic,  
 CC antihemetic, antihypoid, CNS, dermatological, gastrointestinal,  
 CC haemostatic, hepatotrophic, immunostimulant, immunosuppressive, muscular,  
 CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and  
 CC virucide activities, and can be used in gene therapy. The nucleic acid  
 CC (1) and the encoded polypeptides, compositions, kits and methods are  
 CC useful in diagnosing and treating an immune related disease and in  
 CC stimulating an immune response. The present sequence represents a human  
 CC PRO protein from the present invention.

XX Sequence 134 AA;

Query Match 61.8%; Score 430; DB 8; Length 134;  
 Best Local Similarity 64.9%; Pred. No. 6.8e-43;  
 Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNTSLALGAAYVSAVAENPMNRVLAETTLTSTRTWLIDGNLMTPTENKH 60  
 DB 1 MRMLNTSLALGAAYVSAVAENPMNRVLAETTLTSTRTWLIDGNLMTPTENKH 60  
 QY 61 QLCIKVFOGIDTLKNQTAHGAVDKL FQNL SLIKHIEROKKRCAGERRVTKFLDYIQ 120  
 DB 61 QLCIKVFOGIDTLKNQTAHGAVDKL FQNL SLIKHIEROKKRCAGERRVTKFLDYIQ 120  
 QY 121 VFLGVINTEWTPES 134  
 DB 121 VFLGVINTEWTPES 134

RESULT 13  
 AAO30457

ID AAO30457 standard; protein; 285 AA.

XX AAO30457;

XX 22-SEP-2003 (first entry)

XX hIL5-P30-P2-hIL5 (hIL5.34) fusion construct protein.

KW Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;  
 KW tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;  
 KW IL5; epitope; human; tetanus toxoid; chimeric.

OS Homo sapiens.  
 OS Unidentified.  
 OS Chimeric.

Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /note= "Human IL5 leader peptide"  
 FT Protein 20..285  
 FT /note= "Mature hIL5.34 protein"

XX MO2003042244-A2.

XX 22-MAY-2003.

XX 15-NOV-2002; 2002WO-DK000764.

XX 16-NOV-2001; 2001DK-00001702.  
 XX 16-NOV-2001; 2001US-0331575P.

XX (PHAR-) PHARMEXA AS.

XX (KLYS/) KLYSNER S.

XX (NIEL/) NIELSEN F S.

XX (BRAT/) BRATT T.

XX (VOLD/) VOLDORF B.

XX (MOUR/) MOURITSEN S.

XX KLYSNER S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;

DR WPI, 2003-449558/42.  
 DR N-PSDB; AAL61293.

XX New immunogenic analogue of a polymeric protein, useful for preparing a  
 PT composition for treating inflammatory diseases e.g. arthritis.

XX Claim 20; Page 109-110; 196pp; English.

XX The invention relates to immunogenic analogues of multimeric proteins  
 CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis  
 CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic  
 CC analogues. The immunogenic analogue is useful for preparing a composition  
 CC for treating inflammatory diseases, e.g., arthritis. It is also used in  
 CC gene therapy. The present sequence is a fusion construct which comprises  
 CC 2 human interleukin 5 (IL5) monomers joined by tetanus toxoid epitopes  
 CC P30 and P2. This sequence is used to illustrate the method of the  
 CC invention

XX Sequence 285 AA;

Query Match 61.8%; Score 430; DB 6; Length 285;  
 Best Local Similarity 64.9%; Pred. No. 2.1e-42;  
 Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNTSLALGAAYVSAVAENPMNRVLAETTLTSTRTWLIDGNLMTPTENKH 60  
 DB 1 MRMLNTSLALGAAYVSAVAENPMNRVLAETTLTSTRTWLIDGNLMTPTENKH 60  
 QY 61 QLCIKVFOGIDTLKNQTAHGAVDKL FQNL SLIKHIEROKKRCAGERRVTKFLDYIQ 120  
 DB 61 QLCIKVFOGIDTLKNQTAHGAVDKL FQNL SLIKHIEROKKRCAGERRVTKFLDYIQ 120  
 QY 121 VFLGVINTEWTPES 134  
 DB 121 VFLGVINTEWTPES 134

RESULT 14  
 AAO30458

ID AAO30458 standard; protein; 285 AA.

XX AAO30458;

XX 22-SEP-2003 (first entry)

XX hIL5-P2-P30-hIL5 (hIL5.35) fusion construct protein.

KW Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;  
 KW tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;  
 KW IL5; epitope; human; tetanus toxoid; chimeric.

OS Homo sapiens.  
 OS Unidentified.  
 OS Chimeric.

Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /note= "Human IL5 leader peptide"  
 FT Protein 20..285  
 FT /note= "Mature hIL5.35 protein"

XX MO2003042244-A2.

XX 22-MAY-2003.

XX 15-NOV-2002; 2002WO-DK000764.

XX 16-NOV-2001; 2001DK-00001702.  
 XX 16-NOV-2001; 2001US-0331575P.

XX (PHAR-) PHARMEXA AS.

XX (KLYS/) KLYSNER S.

XX (NIEL/) NIELSEN F S.



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## OM protein - protein search, using sw model

Run on: August 4, 2005, 16:59:07 / Search time 26.3695 Seconds  
(without alignments)  
488.938 Million cell updates/sec

Title: US-10-787-382-5  
Perfect score: 696  
Sequence: 1 MRMLNLISLILGAAYSAF.....FLDYLVGLGVINTEWTPES 134

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	551	79.2	134	2 JCS116	interleukin-5 prec
2	430	61.8	134	1 A28477	interleukin-5 prec
3	376	54.0	133	1 ICMS5	interleukin-5 prec
4	361	51.9	132	1 A48418	interleukin-5 prec
5	83.5	12.0	1199	2 G69698	RNA polymerase (be
6	78.5	11.3	258	2 T47758	hypothetical prote
7	77.5	11.1	331	2 G83876	hypothetical prote
8	77	11.1	478	2 T33735	hypothetical prote
9	74.5	10.7	1232	2 B39432	ATP-dependent deox
10	73.5	10.6	253	2 T47757	hypothetical prote
11	72.5	10.4	207	2 C71914	phosphoserine phos
12	72.5	10.4	451	2 S33816	kinasin light chai
13	72.5	10.4	649	2 S33813	kinasin light chai
14	72.5	10.4	677	2 S33814	kinasin light chai
15	72.5	10.4	686	2 S33815	kinasin light chai
16	72	10.3	253	2 C97331	arac-type DNA-bind
17	72	10.3	401	2 S28653	hypothetical prote
18	71	10.2	216	2 B69498	hypothetical prote
19	71	10.2	300	2 F84594	hypothetical prote
20	71	10.2	328	2 F64187	P-aminobenzozate sy
21	71	10.2	446	2 S76228	hypothetical prote
22	71	10.2	461	2 T38698	nocl protein - fis
23	70.5	10.2	544	2 T42932	virion tegument pr
24	70.5	10.1	1055	2 T10432	DNA-directed RNA p
25	70	10.1	215	2 F45355	ORF2 protein - Aut
26	70	10.1	933	2 A59250	myosin - Acetabula
27	70	10.1	1871	2 D96698	probable DNA polym
28	70	10.1	1894	2 T02155	DNA-directed DNA p
29	69.5	10.0	1188	2 JC4889	phosphatidylinosit

30	69	9.9	215	2 B72854	AcOrf-34 protein -
31	69	9.9	346	2 S66958	UBE1 protein - Yea
32	69	9.9	437	2 S50006	preproteins translo
33	69	9.9	759	2 P64662	trans-Golgi membra
34	68.5	9.8	189	2 D89966	truncated transpos
35	68.5	9.8	190	2 S23712	interferon alpha-I
36	68.5	9.8	638	2 AB2115	hypothetical prote
37	68.5	9.8	709	2 T32089	hypothetical prote
38	68.5	9.8	756	2 T12697	NADH2 dehydrogenas
39	68.5	9.8	1192	2 S65235	probable membrane
40	68	9.8	215	2 T41780	AcMNV of134 - Bom
41	68	9.8	304	2 B23431	hypothetical prote
42	68	9.8	414	2 G84311	hypothetical prote
43	68	9.8	416	2 T35282	probable two compo
44	68	9.8	529	2 S35306	phytoene dehydroge
45	68	9.8	767	1 COZPCD	cdci1 start contro
46	68	9.8	1621	2 A82255	hypothetical prote
47	67.5	9.7	247	2 C69272	hypothetical prote
48	67.5	9.7	1189	2 JVB018	SH2-containing ino
49	67	9.6	189	2 IVC01C	interferon alpha-I
50	67	9.6	317	2 G86761	hypothetical prote
51	67	9.6	356	2 S15156	myosin heavy chain
52	67	9.6	437	2 JCS115	preproteins translo
53	67	9.6	463	2 T28748	hypothetical prote
54	67	9.6	520	2 E71416	hypothetical prote
55	67	9.6	570	2 AG1228	DNA polymerase bet
56	67	9.6	2311	2 T06161	acetyl-CoA carboxy
57	66.5	9.6	274	2 T21284	hypothetical prote
58	66.5	9.6	454	2 D86793	drug-export protei
59	66.5	9.6	590	2 H71977	hypothetical prote
60	66.5	9.6	767	2 T37848	SCF complex protei
61	66.5	9.6	1957	2 A59294	skeletal myosin -
62	66	9.5	119	2 G87441	DNA-directed RNA p
63	66	9.5	360	2 F86775	hypothetical prote
64	66	9.5	1197	2 A91035	probable sensor fo
65	66	9.5	1197	2 C85879	probable sensor fo
66	66	9.5	1625	2 T02921	acetyl-CoA carboxy
67	66	9.5	2335	2 T02335	acetyl-CoA carboxy
68	65.5	9.4	248	2 A46552	glucosamine-6-phos
69	65.5	9.4	368	2 A69774	integrase homolog
70	65.5	9.4	583	2 T01470	diphosphate-fructo
71	65.5	9.4	756	2 S40305	multicystatin - po
72	65.5	9.4	2178	2 S55805	alpha-toxin - CloS
73	65.5	9.4	2269	2 T28677	thoxyproy protein -
74	65	9.3	295	2 A69636	glycine-tRNA ligas
75	65	9.3	377	2 AB1991	hypothetical prote
76	65	9.3	538	2 S67766	RNA-export mediato
77	65	9.3	549	2 JC4083	chaperonin - Caeno
78	65	9.3	549	2 T24508	hypothetical prote
79	65	9.3	664	1 JX0336	succinate dehydrog
80	65	9.3	738	1 S51380	protein kinase STB
81	65	9.3	886	1 AD0831	probable acyl-CoA
82	65	9.3	1081	2 S15040	pleiotropic drug r
83	65	9.3	1460	2 T00095	hypothetical prote
84	65	9.3	1685	2 T02750	acetyl-CoA carboxy
85	64.5	9.3	210	2 P64200	chymotrypsin kinase
86	64.5	9.3	220	2 A97953	multidrug efflux p
87	64.5	9.3	225	2 S73585	MG068 homolog D02-
88	64.5	9.3	246	2 E95085	transcription regu
89	64.5	9.3	328	2 B85940	type III secretion
90	64.5	9.3	328	2 P91094	type III secretion
91	64.5	9.3	451	1 JG6180	stearyl-CoA 9-des
92	64.5	9.3	478	2 B90507	gamma-glutamyltran
93	64.5	9.3	479	2 AD1263	two-component sens
94	64.5	9.3	524	2 D960109	T-complex protei
95	64.5	9.3	536	2 D87631	conserved hypochet
96	64.5	9.3	702	2 T12146	NADH2 dehydrogenas
97	64.5	9.3	823	2 G86162	protein P1003.1 [i
98	64.5	9.3	1570	2 AC2012	hypothetical prote
99	64	9.2	155	2 T12777	hypothetical prote
100	64	9.2	212	2 I67408	chorionic somatoma



A/Cross-references: EMBL:X06270; NID:G52687; PIDN:CAA39606.1; PID:G52688  
 R;Kishimoto, T.; Harada, N.; Severinson, E.; Tanabe, T.; Siders, P.; Konishi, M.; Azuma, R.; Nature 324, 70-73, 1986  
 A/Title: Cloning of complementary DNA encoding T-cell replating factor and identity with  
 A/Reference number: A24898; MUID:87065032; PMID:3024009  
 A/Accession: A24898  
 A/Molecule type: mRNA  
 A/Residues: 1-133 <KIN>  
 A/Cross-references: EMBL:X04601; NID:G54898; PIDN:CAA28266.1; PID:G54899  
 R;Mizuta, T.R.; Tanabe, T.; Nakakubo, H.; Noma, T.; Honjo, T.  
 Growth Factors 1, 51-57, 1988  
 A/Title: Molecular cloning and structure of the mouse interleukin-5 gene.  
 A/Reference number: J50077; MUID:90180853; PMID:3078564  
 A/Accession: J50077  
 A/Molecule type: DNA  
 A/Residues: 1-133 <MTZ>  
 R;Takamashi, T.; Yamaguchi, N.; Mita, S.; Yamaguchi, Y.; Suda, T.; Tomimaga, A.; Kikuchi, M.; Immunol. 27, 911-920, 1990  
 A/Title: Structural comparison of murine T-cell (B151K12)-derived T-cell-replating factor  
 A/Reference number: PH0102; MUID:91015093; PMID:2215480  
 A/Accession: PH0102  
 A/Molecule type: protein  
 A/Residues: 21-45; 'X', 47 <TAK>  
 R;Yokota, T.; Coffman, R.L.; Hagiwara, H.; Rennick, D.M.; Takebe, Y.; Yokota, K.; Gemmell, de Vries, J.; Lee, P.D.; Arai, N.; Arai, K.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 7388-7392, 1987  
 A/Title: Isolation and characterization of lymphokine cDNA clones encoding mouse and human  
 A/Reference number: A39881; MUID:88041112; PMID:2823259  
 A/Accession: B39881  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-14, 'AA', 15-133 <YOK>  
 C/Genetics:  
 A/Insertions: 47/3; 58/3; 101/3  
 C/Superfamily: Interleukin-5  
 C/Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell  
 F/1.18/Domain: signal sequence #status predicted <SIG>  
 F/1.19-133/Product: interleukin-5 #status predicted <MAT>  
 F/46/Binding site: carbohydrate (asn) (covalent) #status experimental  
 F/52/Disulfide bonds: interchain (to 104) #status predicted  
 F/55,89/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F/104/Disulfide bonds: interchain (to 62) #status predicted

Query Match 54.0%; Score 376; DB 1; Length 133;  
 Best Local Similarity 56.8%; Pred. No. 8.2e-30;  
 Matches 75; Conservative 21; Mismatches 34; Indels 2; Gaps 1;

Qy 2 RMLNLISLALGAAYVSAFAVENPMNRLVAETLTLSSTRTWLIGDGLMIPPEKNHQ 61  
 Db 3 RMLNLISLALGAAYVSAFAVENPMNRLVAETLTLSSTRTWLIGDGLMIPPEKNHQ 60

Qy 62 LCIEKVFQGITDNLKQTAHGAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYLOV 121  
 Db 61 LCIEKVFQGITDNLKQTAHGAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYLOV 120

Qy 122 FLGVINTEWTPPE 133  
 Db 121 FLGVINTEWTPPE 132

RESULT 4  
 A48418  
 Interleukin-5 precursor - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: A48418; S37641  
 R;Ueberli, K.; Li, W.O.; Qin, Z.H.; Richter, G.; Raabe, T.; Diamantstein, T.; Blankenstein, A.; Nature 372, 81, 1991  
 A/Title: The rat interleukin-5 gene: characterization and expression by retroviral gene  
 A/Reference number: A48418; MUID:91355638; PMID:1653053  
 A/Accession: A48418  
 A/Status: preliminary  
 A/Molecule type: DNA

A/Residues: 1-132 <UBE>  
 A/Cross-references: UNIPROT:Q08125; EMBL:X54419; NID:G313254; PIDN:CAA38283.1; PID:G31325  
 A/Experimental source: cell line TR5-1  
 A/Note: sequence extracted from NCBI backbone (NCBI:63651, NCBI:63652)  
 C/Superfamily: Interleukin-5  
 C/Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell  
 F/1.17/Domain: signal sequence #status predicted <SIG>  
 F/1.18-132/Product: interleukin-5 #status predicted <MAT>  
 F/45,74,88/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F/61/Disulfide bonds: interchain (to 103) #status predicted  
 F/103/Disulfide bonds: interchain (to 61) #status predicted

Query Match 51.9%; Score 361; DB 1; Length 132;  
 Best Local Similarity 54.9%; Pred. No. 2.4e-28;  
 Matches 73; Conservative 21; Mismatches 37; Indels 2; Gaps 1;

Qy 1 RMLNLISLALGAAYVSAFAVENPMNRLVAETLTLSSTRTWLIGDGLMIPPEKNHQ 60  
 Db 1 RMLNLISLALGAAYVSAFAVENPMNRLVAETLTLSSTRTWLIGDGLMIPPEKNHQ 58

Qy 61 QLCIEKVFQGITDNLKQTAHGAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYLO 120  
 Db 59 QLCIEKVFQGITDNLKQTAHGAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYLO 118

Qy 121 FLGVINTEWTPPE 133  
 Db 119 FLGVINTEWTPPE 131

RESULT 5  
 G69698  
 RNA polymerase (beta' subunit) rpoC - Bacillus subtilis  
 C/Species: Bacillus subtilis  
 C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C/Accession: G69698  
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertucci, C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.; Ehrlich, S.D.; Emmerston, P.T.; Eutlian, K.D.; Evington, J.; Fabret, C.; Ferrari, E.  
 Nature 390, 249-256, 1997  
 A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Gallier, lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsreth, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scottore, P.; Sekiguchi, J.; Sekowska, A.; Serot, A.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
 A/Authors: Yoshikawa, H.F.; Zumschein, B.; Yoshikawa, H.; Danchin, A.  
 A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A/Reference number: A69580; MUID:98044033; PMID:9384377  
 A/Accession: G69698  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-1199 <KIN>  
 A/Cross-references: UNIPROT:P37871; GB:299104; GB:AL009126; NID:G2632267; PIDN:CAB11884.1  
 A/Experimental source: strain 168  
 C/Genetics:  
 C/Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 12.0%; Score 83.5; DB 2; Length 1199;  
 Best Local Similarity 27.1%; Pred. No. 7.1;  
 Matches 35; Conservative 20; Mismatches 41; Indels 33; Gaps 6;

Qy 1 RMLNLISLALGAAYVSAFAVENPMNRLVAETLTLSSTRTWLIGDGLMIPPEKNHQ 59  
 Db 114 MGLVDMSPALAEVYFASVYVTPDAN-----TLEKK 147

Qy 60 HQLCIEKVFQGITDNLKQTAHGAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYLO 113  
 Db 148 HQLCIEKVFQGITDNLKQTAHGAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYLO 207

QY 114 KFLDYLOVF 122  
| : : :  
DB 208 KRLEVEAF 216

## RESULT 6

T47758  
hypothetical protein F2413.60 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cross)  
C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C/Accession: T47758

R/Vakutara, G.; Fattmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Welcheselgartner, M.;  
submitted to the Protein Sequence Database, February 2000

A/Reference number: Z24475

A/Accession: T47758

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-258 <NVA>

A/Cross-references: UNIPROT:Q9M1K0; EMBL:AJ138655

A/Experimental source: cultivar Columbia; BAC clone F2413

C/Genetics:

A/Map position: 3

A/Introns: 109/3

A/Note: F2413.60

C/Superfamily: Arabidopsis thaliana hypothetical protein F2413.60

Query Match 11.1%; Score 78.5; DB 2; Length 258;  
Best Local Similarity 26.8%; Pred. No. 3.5;

Matches 22; Conservative 15; Mismatches 38; Indels 7; Gaps 2;

QY 28 RLVAFTLTSLTRTWLIGDGNLMIPPEKNOQLCKRPGQID---TLKQOTAHGEA 83

DB 161 KAVANYISTVSATR---LQNEVWVOISSKIHNFISNVLGILBDRFVLVPMSSRSQ 217

QY 84 VDKLFQNLSTLKEHIEROKKRC 105

DB 218 GERLFTTLHQVKIKENYKLCNC 239

## RESULT 7

G83876  
hypothetical protein BH1815 [imported] - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004

C/Accession: G83876

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A/Reference number: A83650; MUID:20512582; PMID:11058132

A/Accession: G83876

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-331 <STO>

A/Cross-references: UNIPROT:Q9K8V9; GB:AP001513; GB:BA000004; NID:910174345; PIDN:BA0055

A/Experimental source: strain C-125

C/Genetics:

A/Genes: BH1815

Query Match 11.1%; Score 77.5; DB 2; Length 331;  
Best Local Similarity 26.7%; Pred. No. 5.9;

Matches 27; Conservative 20; Mismatches 43; Indels 11; Gaps 4;

QY 7 LSLILA---LGAAYVSAFAVENPMRLVAETLTLLSTRTWLIGDGNLMIPPEKNOQLC 63

DB 86 LRLADALTLTASFLSKETEQMINKLKLTSRLADHL-----DNRLVLP-PDRGNRE-- 137

QY 64 IKQVPGQIDTLKQOTAHGEAVDKLFQNLSTLKEHIEROKKRC 104

DB 138 VOELIKTVHLHDVIRKGEVIRYQGYQNLTKETFLRENGR 178

## RESULT 8

T33735

hypothetical protein H34C03.1 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T33735

R/Kalicki, J.; Gibson, A.

submitted to the EMBL Data Library, October 1998

A/Description: The sequence of C. elegans cosmid H34C03.

A/Reference number: Z21394

A/Accession: T33735

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-478 <PAL>

A/Cross-references: UNIPROT:Q9TYT7; EMBL:AF100662; PIDN:AA068976.1; GSPDB:GN00022; CESP:

A/Experimental source: strain Bristol N2; clone H34C03

C/Genetics:

A/Map position: 4

A/Genes: CESP:H34C03.1

A/Introns: 57/1; 103/2; 185/3; 283/2; 347/3; 426/3

C/Superfamily: Caenorhabditis elegans hypothetical protein H34C03.1

Query Match 11.1%; Score 77; DB 2; Length 478;  
Best Local Similarity 27.3%; Pred. No. 10;

Matches 33; Conservative 20; Mismatches 46; Indels 22; Gaps 5;

QY 6 NLSLALGAAYVSAFAVENPMRLVAETLT---LSTRTWLIGDGNLMIPPEKNOQL 55

DB 261 NMSLLELGMKQOTALALALRLRLSESVTQSEVSAHLKTLVVAAPAPQPVKKIDV 320

QY 56 -----ENKNOQLCKRVEFG---IDTLKQOTAHGEAVDKLFQNLSTLKEHIEROKKRC 104

DB 321 EVKNOQKPEVIVIEKRGERTIDMVFEGTPLSHA-DLSASKSAVARDVLLDSBGR 379

QY 105 C 105

DB 380 C 380

## RESULT 9

B39432  
ATP-dependent deoxyribonuclease chain A adda - Bacillus subtilis

N/Alternate names: ATP-dependent exonuclease synthetase protein Adda

C/Species: Bacillus subtilis

C/Date: 21-Feb-1992 #sequence\_revision 21-Feb-1992 #text\_change 09-Jul-2004

C/Accession: B39432; H69582

R/Koolstra, J.; Venema, G.

J. Bacteriol. 173, 3644-3655, 1991

A/Title: Cloning, sequencing, and expression of Bacillus subtilis genes involved in ATP-

A/Reference number: A39432; MUID:91267926; PMID:1646786

A/Accession: B39432

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1232 <KOO>

A/Cross-references: UNIPROT:P23478; GB:W63489; NID:q142438; PIDN:AAA22201.1; PID:q142440

C/Brion, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi

A.; Ehrlich, S.D.; Emerson, P.T.; Brntlan, K.D.; Birington, J.; Fabre, C.; Ferrari, E.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fume, S.; Galizzi, A.; Gallert

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapilus, A.; Lardinois,

A/Authors: Lauber, U.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maeda, S.; Maesi,

Y., M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,

A/Authors: Schleich, S.; Schreier, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seyer,

akuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Toomari, A.; Tozato, V.; Uchiyama,

T.; Winters, P.; Wilpat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A/Authors: Yoshikawa, H.F.; Zumberstein, E.; Yoshikawa, H.; Darchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: H69582

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1232 <KUN>





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 4, 2005, 16:50:50 ; Search time 121.622 Seconds  
(without alignments)  
554.193 Million cell updates/sec

Title: US-10-787-382-5  
Perfect score: 696  
Sequence: 1 MRMLNLSTLALGAAVSAF.....FLDYLGVLGVINTEWTPES 134

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Uniprot\_03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	100.0	134	1 IL5 CANFA	Q95J76 canis fam1
2	591	84.9	134	1 IL5 FELCA	Q77515 felis silve
3	586	84.2	134	2 Q9TSD7	Q95ed7 felis silve
4	578	83.0	134	2 Q9MTM5	Q9myms sus scrofa
5	571	82.0	118	2 Q9TV10	Q9tv10 canis fam1
6	567	81.5	134	1 IL5 HORSE	O02699 equus cabal
7	551	79.2	134	1 IL5 BOVIN	P52173 bos taurus
8	536	77.0	132	1 IL5 SHEEP	Q28586 ovis aries
9	448	64.4	134	2 Q9MKH1	Q9mkh1 salmuri sci
10	430	61.8	134	1 IL5 HUMAN	P05113 homo sapien
11	429	61.6	134	1 IL5 CERTO	P46685 cercocebus
12	426	61.2	134	1 IL5 MACMU	P48093 macaca mula
13	414.5	59.6	135	1 IL5 CAPRO	O08987 capra hirc
14	388	55.7	132	1 IL5 MERIN	O62575 meriones un
15	388	55.7	132	1 IL5 SIGHT	Q96819 sigmodon hi
16	376	54.0	133	1 IL5 MOUSE	P04401 mus musculu
17	372	53.4	139	1 IL5 MACEV	Q9xt91 macropus eu
18	361	51.9	132	1 IL5 RAT	O08125 rattus norv
19	354	50.9	132	2 Q9R2C9	Q9r2c9 rattus norv
20	214	30.7	48	2 Q6PVS2	Q6pvs2 ovis aries
21	109.5	15.7	40	2 Q9XT92	Q9xt92 smilchopsis
22	98.5	14.2	590	1 NP44_MTXVL	Q9q9q1 myxoma viru
23	84	12.1	360	2 Q62M23	Q62m23 burkholderi
24	84	12.1	360	2 Q63S03	Q63s03 burkholderi
25	83.5	12.0	1199	1 RPOC_BACSU	P37871 bacillus su
26	83	11.9	487	2 Q7R8B3	Q7r8b3 plasmodium
27	81.5	11.7	488	2 Q7ZUN6	Q7zun6 gallus galli
28	80.5	11.6	452	2 Q7SA46	Q7sa46 ashbya gosw
29	80.5	11.6	485	2 Q7ZZZ1	Q7zzz1 gallus galli
30	79.5	11.4	610	2 Q9NA53	Q9na53 caenorhabdi
31	79	11.4	676	2 Q7YKVS	Q7ykv5 mapania par

32	78.5	11.3	258	2 Q9M1K0	Q9m1k0 arabidopsis
33	78.5	11.3	463	2 Q91WC6	Q91wc6 mus musculu
34	78.5	11.3	490	2 Q9JTR0	Q9jtr0 mus musculu
35	77.5	11.1	331	2 Q9KXV9	Q9kxv9 bacillus ha
36	77.5	11.1	721	2 Q7JPE9	Q7jpe9 treponema d
37	77.5	11.1	1199	2 Q65PB4	Q65pb4 bacillus il
38	77	11.1	437	1 SECV_STRGB	Q59912 streptomyces
39	77	11.1	478	2 Q9TYT7	Q9tyt7 caenorhabdi
40	76.5	11.0	158	2 Q96575	Q96575 leucophaea
41	76.5	11.0	266	2 Q6FW99	Q6fw99 candida gla
42	75.5	10.8	284	2 Q8NDP7	Q8ndp7 homo sapien
43	75.5	10.8	490	2 Q8WVP7	Q8wvp7 homo sapien
44	75.5	10.8	490	2 Q96QZ5	Q96qz5 homo sapien
45	75.5	10.8	655	2 Q7MW24	Q7mw24 porphyromon
46	75	10.8	292	2 Q8PUD3	Q8pud3 methanosaar
47	74.5	10.7	313	2 Q8PNY3	Q8pny3 xanthomonas
48	74.5	10.7	1232	1 ADDA_BACSU	P23478 bacillus su
49	74	10.6	241	2 Q8SKT6	Q8skt6 myosotis di
50	74	10.6	241	2 Q8SKX2	Q8skx2 myosotis ra
51	74	10.6	302	2 Q831U2	Q831u2 enterococcu
52	74	10.6	355	2 Q724T8	Q724t8 listeria mo
53	74	10.6	395	2 Q9VKL1	Q9vkl1 drosophila
54	73.5	10.6	161	2 Q6IL05	Q6il05 drosophila
55	73.5	10.6	253	2 Q9M1K1	Q9m1k1 arabidopsis
56	73.5	10.6	1293	2 Q8BEY1	Q8bey1 shewanella
57	73.5	10.6	1835	2 Q6BNW7	Q6bnw7 debaryomyce
58	73	10.5	241	2 Q8SKY3	Q8sky3 myosotis ma
59	73	10.5	248	2 Q8RVK0	Q8rvk0 helianthus
60	73	10.5	313	2 Q8PCA2	Q8pcal xanthomonas
61	73	10.5	623	2 Q7XR41	Q7xral oryza sativ
62	73	10.5	661	2 Q921P5	Q921p5 mus musculu
63	73	10.5	664	1 D9SA_MOUSE	Q8kb25 mus musculu
64	73	10.5	827	2 Q8M3A1	Q8m3a1 oryza sativ
65	72.5	10.4	207	2 Q9ZL12	Q9z112 helicobacte
66	72.5	10.4	229	2 Q9CLP5	Q9cl15 pasteurella
67	72.5	10.4	310	2 Q8ZS22	Q8zsz2 pyrobaculum
68	72.5	10.4	313	2 Q06466	Q06466 xanthomonas
69	72.5	10.4	418	2 Q8SINI	Q8sini oryza sativ
70	72.5	10.4	510	2 Q8GWT4	Q8gwt4 arabidopsis
71	72.5	10.4	611	2 Q6MDA6	Q6mda6 methanococ
72	72.5	10.4	645	2 Q8IHQ8	Q8ihq8 plasmidium
73	72.5	10.4	654	2 Q6DBB3	Q6dbb3 ewingia car
74	72.5	10.4	686	1 KLC_STRPU	Q05090 strongyloce
75	72	10.3	253	2 Q97DG5	Q97dg5 clostridium
76	72	10.3	296	2 Q8TOV4	Q8tov4 methanosaar
77	72	10.3	401	1 Y148_METSM	P22344 methanobrev
78	72	10.3	562	2 Q7TH69	Q7th69 lycoris pot
79	72	10.3	692	2 Q6YK77	Q6yk77 toxoplasma
80	71.5	10.3	239	2 Q7UEK7	Q7uek7 rhodospirill
81	71.5	10.3	534	2 Q7SCW8	Q7scw8 neurospora
82	71.5	10.3	595	2 Q6CS00	Q6cs00 kluyveromyc
83	71.5	10.3	664	2 Q981B2	Q981b2 litelle cher
84	71.5	10.3	823	2 Q9X206	Q9xz06 drosophila
85	71.5	10.3	907	2 Q92KQ9	Q92kz9 rhizobium m
86	71	10.2	216	1 YJ87_ARCFU	Q28222 archaeoglob
87	71	10.2	279	2 Q00944	Q00944 theileria m
88	71	10.2	300	2 Q9SKT0	Q9skt0 arabidopsis
89	71	10.2	328	1 YB70_HAEIN	Q75327 haemophilus
90	71	10.2	446	2 Q7F4390	P79063 synechocyst
91	71	10.2	461	1 T1P1_SCHPO	P79063 synechocyst
92	71	10.2	544	2 Q9YTF7	Q9ytf7 acetivine her
93	71	10.2	827	2 Q8MYT8	Q8myt8 drosophila
94	71	10.2	827	2 Q9W3C9	Q9w3c9 drosophila
95	71	10.2	2321	2 Q947M6	Q947m6 betaria ita
96	70.5	10.1	224	2 Q7PYK6	Q7pyk6 anopheles g
97	70.5	10.1	320	2 Q8TSW7	Q8tsw7 methanosaar
98	70.5	10.1	347	2 Q6N9Z5	Q6n9z5 rhodospirill
99	70.5	10.1	455	2 Q7SRG6	Q7srg6 neurospora
100	70.5	10.1	480	2 Q6IWP4	Q6iwp4 brachydanio

## ALIGNMENTS

```

RESULT 1
IL5_CANFA STANDARD; PRT; 134 AA.
ID 077515; O62740;
AC 077515;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Bosnophil differentiation factor).
GN Name=IL5;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OC NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98452719; PubMed=9781459;
RA Padrid P.A., Qin Y., Wells T.N.C., Solway J., Camoretti-Mercado B.;
RT "Sequence and structural analysis of feline interleukin-5 cDNA.";
RL Am. J. Vet. Res. 59:1263-1269 (1998).
RN [2]
RP SEQUENCE OF 12-128 FROM N.A.
RA Harley R., Day M.J., Gruffydd-Jones T.J., Harbourn D.A., Helps C.R.;
RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC -----
DR EMBL; AF025436; AAC64505.1; -.
DR EMBL; AF051372; AAC05752.1; -.
DR HSSP; P05113; 1HUL.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT CHAIN 20 134 Interleukin-5.
FT SIGNAL 19 By similarity.
FT DISULFID 63 63 Interchain (with C-105) (By similarity).
FT DISULFID 105 105 Interchain (with C-63) (By similarity).
FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
FT CONFLICT 104 105 KC -> NF (in Ref. 2).
FT CONFLICT 108 111 ERRR -> KKKK (in Ref. 2).
FT CONFLICT 114 114 K -> N (in Ref. 2).
FT CONFLICT 117 117 D -> N (in Ref. 2).
FT CONFLICT 121 121 V -> F (in Ref. 2).
FT CONFLICT 125 126 VI -> IL (in Ref. 2).
SQ SEQUENCE 134 AA; 15224 MW; 87D18DB8F8CAG20 CRC64;
Query Match 84.9%; Score 591; DB 1; Length 134;
Best Local Similarity 85.1%; Pred. No. 6; 8e-50;
Matches 114; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

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ID IL5_FELCA STANDARD; PRT; 134 AA.
AC 077515; O62740;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Bosnophil differentiation factor).
GN Name=IL5;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OC NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98452719; PubMed=9781459;
RA Padrid P.A., Qin Y., Wells T.N.C., Solway J., Camoretti-Mercado B.;
RT "Sequence and structural analysis of feline interleukin-5 cDNA.";
RL Am. J. Vet. Res. 59:1263-1269 (1998).
RN [2]
RP SEQUENCE OF 12-128 FROM N.A.
RA Harley R., Day M.J., Gruffydd-Jones T.J., Harbourn D.A., Helps C.R.;
RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF025436; AAC64505.1; -.
DR EMBL; AF051372; AAC05752.1; -.
DR HSSP; P05113; 1HUL.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT CHAIN 20 134 Interleukin-5.
FT SIGNAL 19 By similarity.
FT DISULFID 63 63 Interchain (with C-105) (By similarity).
FT DISULFID 105 105 Interchain (with C-63) (By similarity).
FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
FT CONFLICT 104 105 KC -> NF (in Ref. 2).
FT CONFLICT 108 111 ERRR -> KKKK (in Ref. 2).
FT CONFLICT 114 114 K -> N (in Ref. 2).
FT CONFLICT 117 117 D -> N (in Ref. 2).
FT CONFLICT 121 121 V -> F (in Ref. 2).
FT CONFLICT 125 126 VI -> IL (in Ref. 2).
SQ SEQUENCE 134 AA; 15224 MW; 87D18DB8F8CAG20 CRC64;
Query Match 84.9%; Score 591; DB 1; Length 134;
Best Local Similarity 85.1%; Pred. No. 6; 8e-50;
Matches 114; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

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Db 121 VFLGVINTEWTTMES 134

## RESULT 3

Q9TSD7 PRELIMINARY; PRT; 134 AA.  
 AC Q9TSD7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Interleukin 5.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Vandegriff E., Hughes K.J., O'Reilly K.L.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF068770; AAC27616.1; -  
 DR HSSP; P05113; 1HUL.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR00186; Interleukin\_5.  
 DR Pfam; PF02025; IL5; 1.  
 DR PRINTS; PR00432; INTERLEUKIN5.  
 DR ProDom; PD006721; Interleukin\_5; 1.  
 SQ SEQUENCE 134 AA; 15176 MW; 9A118B78F8C820 CRC64;

Query Match 84.2%; Score 586; DB 2; Length 134;  
 Best Local Similarity 85.0%; Pred. No. 2,1e-49;  
 Matches 113; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 MRMLNLSLALGAAYSAFAPENPMRLVAETLLSTRHTWLDGDMIPPTENKH 60  
 DB 1 MRMLNLSLALGAAYSAFAPENPMRLVAETLLSTRHTWLDGDMIPPTENKH 60  
 QY 61 QLCIKEYFQGITLKNQTAHGAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYIQ 120  
 DB 61 QLCIKEYFQGITLKNQTAHGAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYIQ 120  
 QY 121 VFLGVINTEWTTMES 133  
 DB 121 VFLGVINTEWTTMES 133

## RESULT 4

Q9MTM5 PRELIMINARY; PRT; 134 AA.  
 AC Q9MTM5;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Interleukin-5.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae.  
 NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20130134; PubMed=10663563;  
 RA Sylvia H., Matvienko O., Leonchik A., Alving K., van der Ploeg I.;  
 RT "Molecular cloning, expression, and purification of pig interleukin-5";  
 RT Immunogenetics 51:59-64(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Johnsen C.K., Grondahl-Hansen J., Johansen R., Jungersen G.,

RA Heegaard P.M.H.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ010088; CAB70611.2; -  
 DR EMBL; AJ133452; CAB38328.1; -  
 DR HSSP; P05113; 1HUL.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR00186; Interleukin\_5.  
 DR Pfam; PF02025; IL5; 1.  
 DR PRINTS; PR00432; INTERLEUKIN5.  
 DR ProDom; PD006721; Interleukin\_5; 1.  
 SQ SEQUENCE 134 AA; 15191 MW; B485D562A028A899 CRC64;

Query Match 83.0%; Score 578; DB 2; Length 134;  
 Best Local Similarity 85.1%; Pred. No. 1,3e-48;  
 Matches 114; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MRMLNLSLALGAAYSAFAPENPMRLVAETLLSTRHTWLDGDMIPPTENKH 60  
 DB 1 MRMLNLSLALGAAYSAFAPENPMRLVAETLLSTRHTWLDGDMIPPTENKH 60  
 QY 61 QLCIKEYFQGITLKNQTAHGAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYIQ 120  
 DB 61 QLCIKEYFQGITLKNQTAHGAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYIQ 120  
 QY 121 VFLGVINTEWTTMES 134  
 DB 121 VFLGVINTEWTTMES 134

## RESULT 5

Q9TV10 PRELIMINARY; PRT; 118 AA.  
 AC Q9TV10;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Interleukin-5 (Fragment).  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF091133; AAD46991.1; -  
 DR HSSP; P05113; 1HUL.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR00186; Interleukin\_5.  
 DR Pfam; PF02025; IL5; 1.  
 DR PRINTS; PR00432; INTERLEUKIN5.  
 DR ProDom; PD006721; Interleukin\_5; 1.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 118 AA; 13507 MW; 36A5563DD67C968C CRC64;

Query Match 82.0%; Score 571; DB 2; Length 118;  
 Best Local Similarity 93.8%; Pred. No. 5,3e-48;  
 Matches 106; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 18 SAFAVENPMRLVAETLLSTRHTWLDGDMIPPTENKHOLCIKEYFQGITLKNQ 77  
 DB 6 SAFAVENPMRLVAETLLSTRHTWLDGDMIPPTENKHOLCIKEYFQGITLKNQ 65  
 QY 78 TAHAQAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYIQVFLGVINTEW 130  
 DB 66 TAHAQAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYIQVFLGVINTEW 118

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RESULT 6
ID IL5_HORSE STANDARD; PRT; 134 AA.
AC 002699;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
GN (Bos)ophil differentiation factor).
DN Name=IL5;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxId=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Vandergriff E.V., Horohov D.W.;
RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC -----
DR EMBL; U91947; AAB51382.1; -.
DR HSSP; POS113; 1HUL.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 19
FT CHAIN 1 19 By similarity.
FT DISULFID 63 63 Interchain (with C-105) (By similarity).
FT DISULFID 105 105 Interchain (with C-63) (By similarity).
FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 134 AA; 15081 MW; 2914840B3E7A006D CRC64;

Query Match 81.5%; Score 567; DB 1; Length 134;
Best Local Similarity 83.5%; Pred. No. 1.5e-47;
Matches 111; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MRLMLNLSTLALGAAYVSAFAVENPNRLVAETLTLLSTHRTWLLGDGMLMPTPENKQH 60
DB 1 MRLMLNLSTLALGAAYVSAFAVENPNRLVAETLTLLSTHRTWLLGDGMLMPTPENKQH 60
QY 61 QLCIKVFGQIDITLKNQTAGAENVDLFQNLSTLKEHIEROKRCAGERRVTKFLDYIQ 120
DB 61 QLCIKVFGQIDITLKNQTAGAENVDLFQNLSTLKEHIEROKRCAGERRVTKFLDYIQ 120
QY 121 VFVGINTWTPES 133
DB 121 VFVGINTWTPES 133
QY 122 VFVGINTWTPES 133
DB 122 VFVGINTWTPES 133
QY 123 VFVGINTWTPES 133
DB 123 VFVGINTWTPES 133

RESULT 7
ID IL5_BOVIN STANDARD; PRT; 134 AA.
AC P52173;
DT 01-OCT-1996 (Rel. 34, Created)

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DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
GN (Bos)ophil differentiation factor).
DN Name=IL5;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA TISUE=Blood;
RX MEDLINE=97075944; PubMed=8918267; DOI=10.1016/0378-1119(96)00252-1;
RA Mertens B., Gobright E., Seow H.F.;
RT "The nucleotide sequence of the bovine interleukin-5-encoding cDNA.";
RL Gene 176:273-274(1996).
CC -1- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC -----
DR EMBL; Z67872; CAA91779.1; -.
DR PIR; JCS116; JCS116.
DR HSSP; POS113; 1HUL.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 21
FT CHAIN 1 21 By similarity.
FT DISULFID 63 63 Interchain (with C-105) (By similarity).
FT DISULFID 105 105 Interchain (with C-63) (By similarity).
FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 134 AA; 15229 MW; 0B3A2328BE7431F4 CRC64;

Query Match 79.2%; Score 551; DB 1; Length 134;
Best Local Similarity 79.9%; Pred. No. 5.6e-46;
Matches 107; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 1 MRLMLNLSTLALGAAYVSAFAVENPNRLVAETLTLLSTHRTWLLGDGMLMPTPENKQH 60
DB 1 MRLMLNLSTLALGAAYVSAFAVENPNRLVAETLTLLSTHRTWLLGDGMLMPTPENKQH 60
QY 61 QLCIKVFGQIDITLKNQTAGAENVDLFQNLSTLKEHIEROKRCAGERRVTKFLDYIQ 120
DB 61 QLCIKVFGQIDITLKNQTAGAENVDLFQNLSTLKEHIEROKRCAGERRVTKFLDYIQ 120
QY 121 VFVGINTWTPES 134
DB 121 VFVGINTWTPES 134
QY 122 VFVGINTWTPES 134
DB 122 VFVGINTWTPES 134
QY 123 VFVGINTWTPES 134
DB 123 VFVGINTWTPES 134

RESULT 8
ID IL5_SHEEP STANDARD; PRT; 132 AA.
AC Q28586;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

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DE Interleukin-5 precursor (IL-5) (T-cell replating factor) (TRF)  
 DE (Eosinophil differentiation factor).  
 GN Name:IL5;  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Caprinae; Ovis.  
 NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bryson C.E., Viney E., Brandon M., Boyd A.W.;  
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Snow H.-F., David M.-J., McWaters P.G., Hurst L., Wood P.R.;  
 RT "Cloning of ovine interleukin-5 cDNA."  
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Factor that induces terminal differentiation of late-  
 developing B-cells to immunoglobulin secreting cells (by  
 similarity).  
 CC -1- SUBUNIT: Homodimer; disulfide-linked (by similarity).  
 CC -1- SIMILARITY: Belongs to the IL-5 family.  
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 CC  
 DR EMBL; U17053; AAB60629.1; -;  
 DR EMBL; U17052; AAB60629.1; JOINED.  
 DR EMBL; U35038; AAC95991.1; -;  
 DR HSSP; P05113; 1HTU.  
 DR InterPro: IPR009079; 4 helix cytokine.  
 DR InterPro: IPR000186; Interleukin\_5.  
 DR Pfam: PF02025; IL5; 1.  
 DR PRINTS; PR00432; INTERLEUKINS.  
 DR ProDom; PD006721; Interleukin\_5; 1.  
 KW Cytokine; Glycoprotein; Growth factor; Signal.  
 FT SIGNAL 19  
 FT CHAIN 20 132 Interleukin-5.  
 FT DISUFID 61 132 Interchain (with C-103) (By similarity).  
 FT DISUFID 103 103 Interchain (with C-61) (By similarity).  
 FT CARBOHYD 74 74 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 132 AA; 14974 MW; D783F2B720E249D9 CRC64;  
 Query Match 77.0%; Score 536; DB 1; Length 132;  
 Best Local Similarity 78.8%; Pred. No. 1,6e-44;  
 Matches 104; Conservative 15; Mismatches 13; Indels 0; Gaps 0;  
 QY 3 MLNLISLALGAAYVSAFAVENPNMRLVAETLLSTHRTWLIGDGNLMTPTPENKHO 62  
 DB 1 MHLRLITVALGAAYVCANAVESTMRLVAETLLSTHRTWLIGDGNLMTPTPENKHO 60  
 QY 63 CIREVFGIDITLKNQTAHGAVDLKFONLSLKEHIEROKRCAGERRVYKFLDYLOVF 122  
 DB 61 CIEEVFGIDITLKNQTAHGAVDLKFONLSLKEHIEROKRCAGERRVYKFLDYLOVF 120  
 QY 123 LGVINTWTPES 134  
 DB 121 LGVINTWTPES 132  
 RESULT 9  
 Q8MKH1 PRELIMINARY; PRT; 134 AA.  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Interleukin-5.  
 OS Saimiri sciureus (Common squirrel monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.  
 NCBI\_TaxID=9521;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-y;  
 RA Herand J.M., Lavergne A., Kazanji M.;  
 RT "Molecular cloning, characterization, and quantification of squirrel  
 monkey (Saimiri sciureus) Th1 and Th2 cytokines."  
 RL Immunogenetics 54:20-29(2002).  
 DR EMBL; AF294756; AAK92043.1; -;  
 DR HSSP; P05113; 1HTU.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro: IPR009079; 4 helix cytokine.  
 DR InterPro: IPR000186; Interleukin\_5.  
 DR Pfam: PF02025; IL5; 1.  
 DR PRINTS; PR00432; INTERLEUKINS.  
 DR ProDom; PD006721; Interleukin\_5; 1.  
 SQ SEQUENCE 134 AA; 15210 MW; EAFACCA5DB48767C CRC64;  
 Query Match 64.4%; Score 448; DB 2; Length 134;  
 Best Local Similarity 67.9%; Pred. No. 6,8e-36;  
 Matches 91; Conservative 13; Mismatches 30; Indels 0; Gaps 0;  
 QY 1 MRMLISLALGAAYVSAFAVENPNMRLVAETLLSTHRTWLIGDGNLMTPTPENK 60  
 DB 1 MRMLISLALGAAYVCANAVESTMRLVAETLLSTHRTWLIGDGNLMTPTPENK 60  
 QY 61 QLCIEVFGIDITLKNQTAHGAVDLKFONLSLKEHIEROKRCAGERRVYKFLDYLO 120  
 DB 61 QLCIEVFGIDITLKNQTAHGAVDLKFONLSLKEHIEROKRCAGERRVYKFLDYLO 120  
 QY 121 VFLGINTWTPES 134  
 DB 121 EFLGINTWTPES 134  
 RESULT 10  
 IL5 HUMAN  
 ID IL5 HUMAN STANDARD; PRT; 134 AA.  
 AC P05113; Q13840;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Interleukin-5 precursor (IL-5) (T-cell replating factor) (TRF)  
 DE (Eosinophil differentiation factor) (B cell differentiation factor I).  
 GN Name:IL5;  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8066782; PubMed=3024129;  
 RA Azuma C., Tanabe T., Konishi M., Kinashi T., Noma T., Matsuda F.,  
 RA Yaeita Y., Takatsu K., Hammarstrom L., Smith C.I.F., Severinson E.,  
 RA Honjo T.;  
 RT "Cloning of cDNA for human T-cell replating factor (interleukin-5) and  
 comparison with the murine homologue."  
 RL Nucleic Acids Res. 14:9149-9158(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88059042; PubMed=2824500;  
 RA Tanabe T., Konishi M., Mizuta T., Noma T., Honjo T.;  
 RT "Molecular cloning and structure of the human interleukin-5 gene."  
 RL J. Biol. Chem. 262:16580-16584(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=88016145; PubMed=3498940;  
 RA Campbell H.D., Tucker W.Q.J., Hort Y., Martinson M.B., Mayo G.,  
 RA Clutterbuck E.J., Sanderson C.J., Young I.G.;  
 RT "Molecular cloning, nucleotide sequence, and expression of the gene  
 RT encoding human eosinophil differentiation factor (Interleukin 5).";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6629-6633(1987).  
 RN (4)  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=88041112; PubMed=2823259;  
 RA Yokota K., Coffman R.L., Hagiwara H., Rennick D.M., Takebe Y.,  
 RA Yokota K., Gemelli L., Shrader B., Yang G., Meyerson P., Luh J.,  
 RA Hoy P., Pene J., Briere F., Splice H., Banchereau J., de Vries J.,  
 RA Lee F.D., Araki N., Araki K.;  
 RT "Isolation and characterization of lymphokine cDNA clones encoding  
 RT mouse and human IgA-enhancing factor and eosinophil colony-stimulating  
 RT factor activities: relationship to interleukin 5.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7388-7392(1987).  
 RN (5)  
 RP SEQUENCE FROM N.A.  
 RA Honjo T., Takatsu K., Severinson E.;  
 RA Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.  
 RN (6)  
 RP SEQUENCE FROM N.A.  
 RA Bieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
 RA Nickerson D.A.;  
 RT "SeattleSNP: NHLBI HL66682 program for genomic applications, UW-  
 RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RN (7)  
 RP SEQUENCE OF 20-134, AND DISULFIDE BONDS.  
 RA MEDLINE=90299868; PubMed=2361960;  
 RA Minamide Y., Kodama S., Katayama T., Adachi H., Tanaka S.,  
 RA Tsujimoto M.;  
 RT "Structure of recombinant human interleukin 5 produced by Chinese  
 RT hamster ovary cells.";  
 RL J. Biochem. 107:292-297(1990).  
 RN (8)  
 RP DISULFIDE BONDS.  
 RA MEDLINE=91233878; PubMed=2037074; DOI=10.1016/0014-5793(91)80553-F;  
 RA Proudfoot A.E.I., Davies J.G., Turcatti G., Wingfield P.T.;  
 RT "Human interleukin-5 expressed in *Escherichia coli*: assignment of the  
 RT disulfide bridges of the purified unglycosylated protein.";  
 RL FEBS Lett. 283:61-64(1991).  
 RN (9)  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
 RA MEDLINE=93247642; PubMed=8483502; DOI=10.1038/363172a0;  
 RA Milburn M.V., Hassell A.M., Lambert M.H., Jordan S.R.,  
 RA Proudfoot A.E.I., Graber P., Wells T.N.C.;  
 RT "A novel dimer configuration revealed by the crystal structure at 2.4-  
 RT A resolution of human interleukin-5.";  
 RL Nature 363:172-176(1993).  
 CC -I- FUNCTION: Factor that induces terminal differentiation of late-  
 CC developing B-cells to immunoglobulin secreting cells.  
 CC -I- SUBUNIT: Homodimer; disulfide-linked.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- SIMILARITY: Belongs to the IL-5 family.  
 CC -I- DATAABAS: NAME=Rad Systems' cytokine mini-reviews: IL5;  
 CC WWW=[http://www.rndsystems.com/asp/g\\_siltebuilder.asp?bodyid=207](http://www.rndsystems.com/asp/g_siltebuilder.asp?bodyid=207).  
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 CC -----  
 CC EMBL; X04688; CAA28390.1; -  
 CC EMBL; J03478; AAA74469.1; -  
 CC EMBL; J02971; AAA98620.1; -  
 CC EMBL; X12705; CAA31210.1; -  
 CC EMBL; X12706; CAA31211.1; -  
 CC EMBL; AF532465; AAK19759.1; -

DR PIR; A28477; A28477.  
 DR PDB; 1HUL; X-ray; A/B=24-131.  
 DR Genew; HGNC:6016; IL5.  
 DR MIM; 147850; -  
 DR GO; GO:0005576; Cerebral cellular; TAS.  
 DR GO; GO:0005137; P-interleukin-5 receptor binding; TAS.  
 DR GO; GO:0006266; P-hypersensitive response; TAS.  
 DR GO; GO:0006954; P-inflammatory response; TAS.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR00186; Interleukin\_5.  
 DR Pfam; PF02025; IL5; 1.  
 DR PRINTS; PR00432; INTERLEUKIN5.  
 DR Prodom; PD006721; Interleukin\_5; 1.  
 DR 3D-structure; Cytokine; Direct protein sequencing; Glycoprotein;  
 KW Growth factor; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 134 Interleukin-5.  
 FT DISULFID 63 63 Interchain (with C-105).  
 FT DISULFID 105 105 Interchain (with C-63).  
 FT CARBOHYD 22 22 O-linked.  
 FT CARBOHYD 47 47 N-linked (GlcNAc...)  
 FT CONFLICT 88 88 N-linked (GlcNAc...)  
 FT HELIX 26 38 F -> L (in Ref. 5; CAA31210).  
 FT TURN 39 40  
 FT TURN 41 45  
 FT HELIX 46 46  
 FT TURN 51 54  
 FT STRAND 60 62  
 FT HELIX 64 77  
 FT HELIX 82 82  
 FT TURN 83 103  
 FT TURN 104 105  
 FT STRAND 108 111  
 FT HELIX 112 128  
 FT TURN 129 129  
 SQ SEQUENCE 134 AA; 15238 MW; DC984467179556A3 CRC64;  
 Query Match 61.8%; Score 430; DB 1; Length 134;  
 Best Local Similarity 64.9%; Pred. No. 3.9e-34;  
 Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;  
 QY 1 MMLNLSTLALGAAYVSAFAVENPMNRVARTLTLSHRTMLGDNLMITPENKRN 60  
 DB 1 MMLNLSTLALGAAYVAIPTEIPTSALVKSTLALSTRTLTLANETRLVPPVKRN 60  
 QY 61 QLCIKVFOGIDTLKQNTAGBAVDLFPQNLILKIHIEROKRCAGERRVYTKFLDYIQ 120  
 DB 61 QLCIBEIFGIGTIGLESQTVGGIVRLFKNLGILKKYIDGQKKKGERRRVNQFLDYIQ 120  
 QY 121 VFLGVINTEWTPES 134  
 DB 121 EFLGVINTEWTPES 134  
 RESULT 11  
 IL5\_CERTO  
 ID IL5\_CERTO STANDARD; PRT; 134 AA.  
 AC P4685;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
 DE (Eosinophil differentiation factor).  
 GN Name:IL5;  
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 ON NCBI\_Taxid=9531;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FUJ;  
 RX MEDLINE=96003435; PubMed=7561102;

RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;  
 RT "Comparative sequence analysis of cytokine genes from human and  
 nonhuman primates";  
 RL J. Immunol. 155:3946-3954(1995).  
 CC -1- FUNCTION: Factor that induces terminal differentiation of late-  
 developing B-cells to immunoglobulin secreting cells (By  
 similarity).  
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the IL-5 family.  
 CC -----  
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 CC -----  
 DR EMBL; L26033; AAA99971.1; -.  
 DR HSSP; P05113; 1HUL.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR000186; Interleukin\_5.  
 DR Pfam; PF02025; IL5; 1.  
 DR PRINTS; PR00432; INTERLEUKINS.  
 DR Prodom; PD006721; Interleukin\_5; 1.  
 KW Cytokine; Glycoprotein; Growth factor; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 1 19 By similarity.  
 FT DISULFID 20 134 Interleukin-5.  
 FT DISULFID 63 63 Interchain (with C-105) (By similarity).  
 FT DISULFID 105 105 Interchain (with C-63) (By similarity).  
 FT CARBOHYD 22 22 O-linked (By similarity).  
 FT CARBOHYD 47 47 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 134 AA; 15339 MW; 7BDD491C437981BD CRC64;  
 Query Match 61.6%; Score 429; DB 1; Length 134;  
 Best Local Similarity 64.2%; Pred. No. 4.9e-34;  
 Matches 86; Conservative 20; Mismatches 28; Indels 0; Gaps 0;  
 QY 1 MRRLNLISLALGAAYVSAFVNPNNRLVAETLTLLSTRHWLIGDGNIMIPPEKNH 60  
 DB 1 MRRLNLISLALGAAYVSAFVNPNNRLVAETLTLLSTRHWLIGDGNIMIPPEKNH 60  
 QY 61 QLCIKVFGQIDTLKNOTANGAVDKLFONSLIKHEIRKRCGGERRRVTKFLDYIQ 120  
 DB 61 QLCIKVFGQIDTLKNOTANGAVDKLFONSLIKHEIRKRCGGERRRVTKFLDYIQ 120  
 QY 121 VPLGVNTEWTPES 134  
 DB 121 EPLGVNTEWTPES 134  
 Db 121 EPLGVNTEWTPES 134

RESULT 12  
 IL5\_MACMU STANDARD; PRT; 134 AA.  
 AC P48093;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
 DE (eosinophil differentiation factor).  
 GN Name=IL5;  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=96003435; PubMed=7561102;  
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;

RT "Comparative sequence analysis of cytokine genes from human and  
 nonhuman primates";  
 RL J. Immunol. 155:3946-3954(1995).  
 CC -1- FUNCTION: Factor that induces terminal differentiation of late-  
 developing B-cells to immunoglobulin secreting cells (By  
 similarity).  
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the IL-5 family.  
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 CC -----  
 DR EMBL; U19848; AAA86710.1; -.  
 DR HSSP; P05113; 1HUL.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR000186; Interleukin\_5.  
 DR Pfam; PF02025; IL5; 1.  
 DR PRINTS; PR00432; INTERLEUKINS.  
 DR Prodom; PD006721; Interleukin\_5; 1.  
 KW Cytokine; Glycoprotein; Growth factor; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 1 19 By similarity.  
 FT DISULFID 20 134 Interleukin-5.  
 FT DISULFID 63 63 Interchain (with C-105) (By similarity).  
 FT DISULFID 105 105 Interchain (with C-63) (By similarity).  
 FT CARBOHYD 22 22 O-linked (By similarity).  
 FT CARBOHYD 47 47 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 134 AA; 15150 MW; DC985ECF4B8B86A3 CRC64;  
 Query Match 61.2%; Score 426; DB 1; Length 134;  
 Best Local Similarity 64.9%; Pred. No. 9.7e-34;  
 Matches 87; Conservative 16; Mismatches 31; Indels 0; Gaps 0;  
 QY 1 MRRLNLISLALGAAYVSAFVNPNNRLVAETLTLLSTRHWLIGDGNIMIPPEKNH 60  
 DB 1 MRRLNLISLALGAAYVSAFVNPNNRLVAETLTLLSTRHWLIGDGNIMIPPEKNH 60  
 QY 61 QLCIKVFGQIDTLKNOTANGAVDKLFONSLIKHEIRKRCGGERRRVTKFLDYIQ 120  
 DB 61 QLCIKVFGQIDTLKNOTANGAVDKLFONSLIKHEIRKRCGGERRRVTKFLDYIQ 120  
 QY 121 VPLGVNTEWTPES 134  
 DB 121 EPLGVNTEWTPES 134  
 Db 121 EPLGVNTEWTPES 134

RESULT 13  
 IL5\_CAVPO STANDARD; PRT; 135 AA.  
 AC O08587;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
 DE (eosinophil differentiation factor).  
 GN Name=IL5;  
 OS Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96289181; PubMed=8764226;  
 RA Mansourn M., Karmilowicz M., Hawrylik S.J., Malcerio B., Angilly J.,  
 Conklyn M.J., Lilly C.M., Drazen J.M., Lee S.B., Auperin D.D.,  
 de Wet J.R., Cohen V.L., Showell H.J., Danley D.E.;  
 "Production and characterization of guinea pig IL-5 in baculovirus-

RT infected insect cells." ;  
 RL Am. J. Physiol. 270:L1002-L1007(1996).  
 CC -1- FUNCTION: Factor that induces terminal differentiation of late-  
 CC developing B-cells to immunoglobulin secreting cells (By  
 CC similarity).  
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the IL-5 family.  
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 CC -----  
 DR EMBL: U34588; AA061357.1; -.  
 DR HSSP: P05113; 1H0U.  
 DR InterPro: IPR009079; 4\_helix\_cytokine.  
 DR InterPro: IPR00186; Interleukin\_5.  
 DR Pfam: PF02025; IL5; 1.  
 DR PRINTS: PR00432; INTERLEUKINS.  
 DR ProDom: PD006721; Interleukin\_5; 1.  
 DR Cytokine; Glycoprotein; Growth factor; Signal.  
 FT CHAIN 1 19  
 FT SIGNAL 1 19  
 FT FT 20 135  
 FT DISULFID 64 64 Interchain (with C-106) (By similarity).  
 FT DISULFID 106 106 Interchain (with C-64) (By similarity).  
 FT CARBOHYD 48 48 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 77 77 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 91 91 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 135 AA; 15291 MW; EB8525232P52731 CRC64;  
 Query Match 59.6%; Score 414.5; DB 1; Length 135;  
 Best Local Similarity 64.9%; Pred. No. 13e-32;  
 Matches 87; Conservative 14; Mismatches 32; Indels 1; Gaps 1;  
 QY 1 MEMLTSLALGAAYVSAFAVEN-PNNRLVARTLTTLSTRTWLIGDGLMIPTEPNKH 59  
 DB 1 MNTLQGLLALGAVCVCAIPKQSATLRALVRETLTLSTRTWLIGDGLMIPTEPNKH 60  
 QY 60 HOLCIKEVFGIDTLNKGTAHGAVDKLFONTSLIKHEIRKRCAGERRVTKFLDYQ 119  
 DB 61 HOLCIKEIFGIDTLNKGTAHGAVDKLFONTSLIKHEIRKRCAGERRVTKFLDYQ 120  
 QY 120 QVFLGVINTETPE 133  
 DB 121 QEFLLAVINTEWTE 134  
 RESULT 14  
 ID IL5\_MERUN STANDARD; PRT; 132 AA.  
 AC Q62575;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
 DE (Eosinophil differentiation factor).  
 GN Name=IL5;  
 OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).  
 OC Burkaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;  
 OC Meriones.  
 NCBI\_TaxID=10047;  
 RN NCBI\_TaxID=10047;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Mei Z., Klei T.R.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Factor that induces terminal differentiation of late-  
 CC developing B-cells to immunoglobulin secreting cells (By

CC similarity).  
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the IL-5 family.  
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 CC -----  
 DR EMBL: U3780; AA065675.1; -.  
 DR HSSP: P05113; 1H0U.  
 DR InterPro: IPR009079; 4\_helix\_cytokine.  
 DR InterPro: IPR00186; Interleukin\_5.  
 DR Pfam: PF02025; IL5; 1.  
 DR PRINTS: PR00432; INTERLEUKINS.  
 DR ProDom: PD006721; Interleukin\_5; 1.  
 DR Cytokine; Glycoprotein; Growth factor; Signal.  
 FT CHAIN 1 17  
 FT SIGNAL 1 17  
 FT FT 18 132  
 FT DISULFID 61 61 Interchain (with C-103) (By similarity).  
 FT DISULFID 103 103 Interchain (with C-61) (By similarity).  
 FT CARBOHYD 45 45 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 74 74 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 132 AA; 15164 MW; 60CE3852F9F84261 CRC64;  
 Query Match 55.7%; Score 388; DB 1; Length 132;  
 Best Local Similarity 59.4%; Pred. No. 5e-30;  
 Matches 79; Conservative 21; Mismatches 31; Indels 2; Gaps 1;  
 QY 1 MEMLTSLALGAAYVSAFAVENPNNRLVARTLTTLSTRTWLIGDGLMIPTEPNKH 60  
 DB 1 MNTLQGLLALGAVCVCAIPKQSATLRALVRETLTLSTRTWLIGDGLMIPTEPNKH 59  
 QY 61 QLCIKVFGIDTLNKGTAHGAVDKLFONTSLIKHEIRKRCAGERRVTKFLDYQ 120  
 DB 59 QLCIKVFGIDTLNKGTAHGAVDKLFONTSLIKHEIRKRCAGERRVTKFLDYQ 118  
 QY 121 VFLGVINTETPE 133  
 DB 119 EFLGVINTEWTE 131  
 RESULT 15  
 ID IL5\_SIGHI STANDARD; PRT; 132 AA.  
 AC Q9ES19;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
 DE (Eosinophil differentiation factor).  
 GN Name=IL5;  
 OS Sigmodon hispidus (Hispid cotton rat).  
 OC Burkaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Sigmodon.  
 NCBI\_TaxID=42415;  
 RN NCBI\_TaxID=42415;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX PubMed:11054577; DOI=10.1016/S0378-1119(00)00366-8;  
 RA Howard S., Jaquet A., Haumont M., Damme V., Millican F., Glineur F.,  
 RA Bollen A.;  
 RT "Cloning, expression and purification of recombinant cotton rat  
 RT Interleukin-5." ;  
 RL Gene 257:149-155(2000).  
 CC -1- FUNCTION: Factor that induces terminal differentiation of late-  
 CC developing B-cells to immunoglobulin secreting cells.

```

CC -1 SUBUNIT: Homodimer; disulfide-linked.
CC -1 SUBCELLULAR LOCATION: Secreted.
CC -1 SIMILARITY: Belongs to the IL-5 family.
-----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on items
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi-sib.ch).
CC -----
DR EMBL: AF148211; AAG16722.1; -.
DR HSSP: P05113; 1HTL.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR000186; Interleukin_5.
DR Pfam: PF02025; IL5; 1.
DR PRINTS: PR00432; INTERLEUKIN5.
DR ProDom: PD06721; Interleukin-5.
KM Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 132 Interleukin-5.
FT DISULFID 61 61 Interchain (with C-103) (By similarity).
FT DISULFID 103 103 Interchain (with C-61) (By similarity).
FT CARBOHYD 45 45 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 74 74 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 132 AA; 15434 MW; B378B81B3371FEB9 CRC64;

Query Match 55.7%; Score 388; DB 1; Length 132;
Best Local Similarity 59.4%; Pred. No. 5e-30; Indels 2; Gaps 1;
Matches 79; Conservative 19; Mismatches 33;

QY 1 MRMLINTSLALGAAVYSAFVENVNRLVAETLLTSLSTRFTWVLIGDNLMIPTPEKNKH 60
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 1 MRMLLHLSITLV--ACVWTFPAVEIPMHVTFVETLLIGLSTHRTALLTSNETVRLPVPYTKNH 58

QY 61 QLCIKVEVQGITLTKNQTAHGBANDKLFQNTSLIKYHIEROKRCACGRMYATKFLDTLQ 120
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 59 QLCIGELIFRGDILDKNQTVRGIVETTLFQNTSLIKYKIDRQKKGESRRRTROFLDTLQ 118

QY 121 VFLGVINTEWTPR 133
   |||||:::|||||
Db 119 EFLGVGWTEWTPR 131

```

Search completed: August 4, 2005, 17:11:05  
Job time : 126.622 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: August 4, 2005, 16:50:05 ; Search time 115.462 Seconds

(without alignments)  
385.213 Million cell updates/sec

Title: US-10-787-382-10

Perfect score: 610

Sequence: 1 FAVENPMNRRLVAETLTLLST.....FLDYLGVLGVINTEPTES 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

## Database :

A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	610	100.0	115	3	AAV58220 Canine ma
2	610	100.0	134	3	AAV58219 Canine in
3	601	98.5	134	4	AAV72615 Canine in
4	487	79.8	132	2	AAW08479 Ovine IL-
5	358	58.7	115	8	ADL89254 Human mod
6	357	58.5	113	1	AAV93152 Sequence
7	357	58.5	115	8	ADL89235 Human mod
8	357	58.5	287	6	AAO30459 Human mod
9	356	58.4	112	1	AAV80279 Pletiotrop
10	356	58.4	115	3	AAV81038 Sequence
11	356	58.4	115	1	AAV84589 Human int
12	356	58.4	115	5	ABG94295 Human mat
13	356	58.4	115	5	ABG80607 Human mat
14	356	58.4	115	6	AAO30453 Human mat
15	356	58.4	115	7	ADK17208 Human int
16	356	58.4	115	8	ADL89253 Human mod
17	356	58.4	115	8	ADL89261 Human mod
18	356	58.4	115	8	ADL88874 Human cyt
19	356	58.4	115	8	ADL89246 Human mod
20	356	58.4	115	8	ADL89246 Human mod
21	356	58.4	115	8	ADL89255 Human mod
22	356	58.4	123	5	ABG94353 Human C-I
23	356	58.4	123	5	ABG80665 Human IL-
24	356	58.4	123	7	ADK17224 Human C-I
25	356	58.4	134	2	AAV92802 Human int

26	356	58.4	134	4	AAV72617 Human int
27	356	58.4	134	5	ABG94294 Human int
28	356	58.4	134	5	ABG80606 Human pre
29	356	58.4	134	5	AAU10353 Interleuk
30	356	58.4	134	7	ADP70849 Human int
31	356	58.4	134	7	ADK17207 Human int
32	356	58.4	134	8	ADP56010 Human PRO
33	356	58.4	136	5	ABG94352 Human C-I
34	356	58.4	136	5	ABG80664 Human ILn
35	356	58.4	136	7	ADK17223 Human C-I
36	356	58.4	138	5	ABG94351 Human C-I
37	356	58.4	138	5	ABG80663 Human ILn
38	356	58.4	138	7	ADK17222 Human C-I
39	356	58.4	285	6	AAO30457 Human C-I
40	356	58.4	285	6	AAO30458 Human C-I
41	356	58.4	287	6	AAO30460 Human C-I
42	355	58.2	115	8	ADL89251 Human mod
43	355	58.2	115	8	ADL89262 Human mod
44	355	58.2	115	8	ADL89247 Human mod
45	355	58.2	115	8	ADL89241 Human mod
46	355	58.2	115	8	ADL89234 Human mod
47	355	58.2	115	8	ADL89263 Human mod
48	354	58.0	115	8	ADL89248 Human mod
49	354	58.0	115	8	ADL89252 Human mod
50	354	58.0	115	8	ADL89242 Human mod
51	353	57.9	115	8	ADL89243 Human mod
52	353	57.9	115	8	ADL89256 Human mod
53	353	57.9	115	8	ADL89264 Human mod
54	352	57.7	115	8	ADL89260 Human mod
55	352	57.7	115	8	ADL89249 Human mod
56	352	57.7	115	8	ADL89238 Human mod
57	352	57.7	134	5	AAU10354 Interleuk
58	351	57.5	115	8	ADL89239 Human mod
59	351	57.5	115	8	ADL89250 Human mod
60	351	57.5	115	8	ADL89259 Human mod
61	351	57.5	115	8	ADL89245 Human mod
62	351	57.5	115	8	ADL89244 Human mod
63	351	57.5	115	8	ADL89258 Human mod
64	351	57.5	115	8	ADL89265 Human mod
65	351	57.5	115	8	ADL89257 Human mod
66	351	57.5	115	8	ADL89266 Human mod
67	351	57.5	121	2	AAW43436 Human int
68	348	57.0	115	8	ADL89236 Human mod
69	348	57.0	115	8	ADL89237 Human mod
70	347	56.9	115	2	AAW05273 N-termina
71	347	56.9	115	2	AAW72948 Truncated
72	347	56.9	133	1	AAV71064 Murine eo
73	347	56.9	133	1	AAV82969 B cell di
74	347	56.9	133	2	AAV89693 T cell re
75	347	56.9	133	2	AAV72947 T cell re
76	347	56.9	133	2	AAV72618 Murine in
77	347	56.9	133	4	AAV72618 Murine in
78	347	56.9	134	5	ABG94349 Mouse C-I
79	347	56.9	134	5	ABG80661 Mouse IL-
80	347	56.9	134	7	ADK17220 Mouse C-I
81	346	56.7	134	1	AAV81056 Sequence
82	344	56.4	136	5	ABG94348 Mouse C-I
83	344	56.4	136	5	ABG80660 Mouse IL-
84	344	56.4	136	7	ADK17219 Mouse C-I
85	343	56.2	84	4	AAV72616 Canine in
86	343	56.2	84	4	AAW05274 N-termina
87	343	56.2	113	5	ABG94296 Mouse int
88	343	56.2	113	5	ABG80608 Mouse int
89	343	56.2	113	7	ADK17209 Mouse int
90	343	56.2	115	8	ADL89268 Human mod
91	343	56.2	121	1	ABG94350 Mouse C-I
92	343	56.2	121	5	ABG80662 Mouse IL-
93	343	56.2	121	2	AAV05275 N-termina
94	342	56.1	112	2	AAV05275 N-termina
95	342	56.1	115	8	ADL89267 Human mod
96	339	55.6	126	3	AAV45494 Modified
97	335	54.9	132	3	AAV45498 Modified
98	332.5	54.5	126	3	AAV45490 Modified

99 332.5 54.5 126 3 AAB45514 Modified  
100 331.5 54.3 132 3 AAB45520 Modified

## ALIGNMENTS

RESULT 1  
ID AAY58220 standard; protein; 115 AA.

XX AAY58220;

XX 14-MAR-2000 (first entry)

XX Canine mature interleukin-5 (IL-5).

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;

XX Immunoregulation; tumour; cancer; autoimmune disease; vaccine.

XX Canis familiaris.

XX MO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99MO-US011942.

XX 29-MAY-1998; 98US-0087306P.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Drelitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

XX N-PSDB; AAZ55550, AAZ55551.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,

XX useful for treating or preventing e.g. tumors or autoimmune disease.

XX Claim 3b; Page 227; 264pp; English.

XX Sequences AAY58219-Y58220 represent encoded and mature canine interleukin  
XX -5 (IL-5). The invention relates to canine IL-4, canine or feline Flt-3  
XX ligand, canine or feline CD40, canine or feline CD134 (CD40 ligand),  
XX canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline  
XX granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides  
XX which encode these immunoregulatory proteins. The proteins, their  
XX associated nucleic acids, specific antibodies and inhibitors may be used  
XX as vaccines for therapeutic or prophylactic regulation of an immune  
XX response in animals (particularly cats, dogs, horses and humans). They  
XX may be used to treat autoimmune or infectious diseases including  
XX allergies, tumours, inflammation and graft rejection, and to increase the  
XX response from a co-administered antigen. The nucleotide sequences can  
XX also be used for the recombinant production of a protein, while  
XX nucleotide fragments are useful as probes, as amplification primers and  
XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
XX The proteins may be used to raise antibodies and to screen for modulators  
XX of activity, while the antibodies may be used in detection, and in drug  
XX targeting

XX Sequence 115 AA;

XX Query Match 100.0%; Score 610; DB 3; Length 115;

XX Best Local Similarity 100.0%; Pred. No. 2, 6e-64; Indels 0; Gaps 0;

XX Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPMNRLVAETLLSTHRTWLIGDGNLMIPTPENKNHOLCIKEVFGIDITLKNQTA 60

Db 1 FAVENPMNRLVAETLLSTHRTWLIGDGNLMIPTPENKNHOLCIKEVFGIDITLKNQTA 60

QY 61 HGEAVDKLFONTSLIKHIEROKRCAGGRWRYTKFLDYQVFLGVINTWPTES 115

Db 61 HGEAVDKLFONTSLIKHIEROKRCAGGRWRYTKFLDYQVFLGVINTWPTES 115

RESULT 2  
ID AAY58219 standard; protein; 134 AA.

XX AAY58219;

XX 14-MAR-2000 (first entry)

XX Canine interleukin-5 (IL-5).

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;

XX Immunoregulation; tumour; cancer; autoimmune disease; vaccine.

XX Canis familiaris.

XX MO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99MO-US011942.

XX 29-MAY-1998; 98US-0087306P.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Drelitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

XX N-PSDB; AAZ55546, AAZ55547, AAZ55548, AAZ55549.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,

XX useful for treating or preventing e.g. tumors or autoimmune disease.

XX Claim 3b; Page 224; 264pp; English.

XX Sequences AAY58219-Y58220 represent encoded and mature canine interleukin  
XX -5 (IL-5). The invention relates to canine IL-4, canine or feline Flt-3  
XX ligand, canine or feline CD40, canine or feline CD134 (CD40 ligand),  
XX canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline  
XX granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides  
XX which encode these immunoregulatory proteins. The proteins, their  
XX associated nucleic acids, specific antibodies and inhibitors may be used  
XX as vaccines for therapeutic or prophylactic regulation of an immune  
XX response in animals (particularly cats, dogs, horses and humans). They  
XX may be used to treat autoimmune or infectious diseases including  
XX allergies, tumours, inflammation and graft rejection, and to increase the  
XX response from a co-administered antigen. The nucleotide sequences can  
XX also be used for the recombinant production of a protein, while  
XX nucleotide fragments are useful as probes, as amplification primers and  
XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
XX The proteins may be used to raise antibodies and to screen for modulators  
XX of activity, while the antibodies may be used in detection, and in drug  
XX targeting

XX Sequence 134 AA;

XX Query Match 100.0%; Score 610; DB 3; Length 134;

XX Best Local Similarity 100.0%; Pred. No. 3, 2e-64; Indels 0; Gaps 0;

XX Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPMNRLVAETLLSTHRTWLIGDGNLMIPTPENKNHOLCIKEVFGIDITLKNQTA 60

Db 20 FAVENPMNRLVAETLLSTHRTWLIGDGNLMIPTPENKNHOLCIKEVFGIDITLKNQTA 79

QY 61 HGEAVDKLFONTSLIKHIEROKRCAGGRWRYTKFLDYQVFLGVINTWPTES 115

Db 80 HGEAVDKLFONTSLIKHIEROKRCAGGRWRYTKFLDYQVFLGVINTWPTES 134

RESULT 3

AAB72615  
ID AAB72615 standard; protein; 134 AA.  
XX  
AC AAB72615;  
XX  
DT 04-MAY-2001 (first entry)  
XX  
DE Canine interleukin-5 protein #1.  
XX  
KM Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;  
KM inflammatory reaction.  
XX  
OS Canis sp.  
XX  
PN WO200111049-A2.  
XX  
PD 15-FEB-2001.  
XX  
PF 09-AUG-2000; 2000MO-US021651.  
XX  
PR 10-AUG-1999; 99US-00371615.  
XX  
PS (IDEX-) IDEXX LAB INC.  
XX  
PI Guo H, Lawton R, Mexmer B, Aiyappa AP;  
XX  
DR WPI: 2001-191542/19.  
XX  
DR N-PSDB; AAF74300.  
XX  
PT Novel canine interleukin 5 polynucleotide and polypeptides are used for  
XX  
PT generating antibodies which are useful in treating allergies in dogs.  
XX  
PS Claim 29; Page 46-47; 48pp; English.  
XX  
CC The present invention provides the protein and coding sequences of the  
XX  
CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,  
XX  
CC cancer and inflammatory reactions in dogs. The present sequence is one  
XX  
CC version of the IL-5 protein shown in the specification  
XX  
SQ Sequence 134 AA;  
XX  
Query Match 98.5%; Score 601; DB 4; Length 134;  
Best Local Similarity 99.1%; Pred. No. 3.8e-63;  
Matches 114; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 1 PAVENPMNRLLVAETLTLLSTHRTWLIGDGNLMIPTPENKXHQLCIKVFGSIDTLKNOTA 60  
DB 20 PAVENPMNRLLVAETLTLLSTHRTWLIGDGNLMIPTPENKXHQLCIKVFGSIDTLKNOTA 79  
XX  
QY 61 GGEAVNDLFPONLSIKHEIRÖKRCGGERWRVTKFLDYLOVPLGVINTETWPS 115  
DB 80 GGEAVNDLFPONLSIKHEIRÖKRCGGERWRVTKFLDYLOVPLGVINTETWPS 134  
XX  
RESULT 4  
ID AAM08479 standard; protein; 132 AA.  
XX  
AC AAM08479;  
XX  
DT 17-OCT-2003 (revised)  
DT 24-SEP-1997 (first entry)  
XX  
DE Ovine IL-5.  
XX  
KM Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;  
KM livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;  
KM immunosuppression; allergy; reproductive system; growth; early maturity;  
KM antibody; diagnosis; immunopotentiator;  
KM early haematopoietic progenitor cell; cytotoxic cell; thymocyte;  
KM secretion; IGM; IGA; bacterial endotoxin; gamma-interferon.  
XX  
OS Ovis aries.

XX  
PN WO9700321-A1.  
XX  
PD 03-JAN-1997.  
XX  
PF 14-JUN-1996; 96MO-AU000360.  
XX  
PR 14-JUN-1995; 95AU-00003502.  
XX  
PR 27-OCT-1995; 95AN-00006244.  
XX  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
XX  
PI Seow H, Wood P;  
XX  
DR WPI: 1997-077528/07.  
XX  
DR N-PSDB; AAT50755, AAT50756.  
XX  
PT Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine  
XX  
PT adjuvants and to treat or prevent microbial infections in livestock.  
XX  
PS Claim 31; Page 39-40; 78pp; English.  
XX  
CC This protein sequence represents ovine interleukin-5 (IL-5). Ovine IL-5  
XX  
CC or IL-12 are used to treat and/or prevent infections in livestock (esp.  
XX  
CC cows and sheep), particularly where the animals are stressed, e.g. during  
XX  
CC transport. IL-5 and IL-12 can also be used as adjuvants in vaccines for  
XX  
CC veterinary use (partic. weakly immunogenic subunit or synthetic peptide  
XX  
CC vaccines). They may also be used to treat cancer, immunosuppression and  
XX  
CC allergy, to enhance/suppress the reproductive system and to promote  
XX  
CC growth or early maturity. Optionally interleukin can be delivered from  
XX  
CC constructs or delivery cells and antibodies are useful in enzyme  
XX  
CC immunoassays for rapid diagnosis of infection. The interleukins are  
XX  
CC immunopotentiators, especially IL-5 promotes growth of early  
XX  
CC haematopoietic progenitor cells and generation of cytotoxic cells from  
XX  
CC thymocytes, also it stimulates production and secretion of Igm and Iga  
XX  
CC (in synergism with bacterial endotoxin). IL-12 induces production of  
XX  
CC gamma-interferon by, and proliferation of, T and NK cells and increases  
XX  
CC the (non-)specific cytolytic lymphocyte response. The genetic constructs  
XX  
CC can also be used for in vitro production of IL-5 or -12. (updated on 17-  
XX  
CC OCT-2003 to standardise OS field)  
XX  
SQ Sequence 132 AA;  
XX  
Query Match 79.8%; Score 487; DB 2; Length 132;  
Best Local Similarity 80.7%; Pred. No. 1.4e-49;  
Matches 92; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
XX  
QY 2 AVENPMNRLLVAETLTLLSTHRTWLIGDGNLMIPTPENKXHQLCIKVFGSIDTLKNOTA 61  
DB 19 AVSTNRRLVAETLTLLSTHRTWLIGDGNLMIPTPHNTNQLCIEVFGSIDTLKNOTA 78  
XX  
QY 62 GGEAVNDLFPONLSIKHEIRÖKRCGGERWRVTKFLDYLOVPLGVINTETWPS 115  
DB 79 GDAVKKIFRNLSIKHEYIDLÖKRRCGGERWRVTKFLDYLOVPLGVINTETWPS 132  
XX  
RESULT 5  
ID ADL89254 standard; protein; 115 AA.  
XX  
AC ADL89254;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human modified cytokine protein #536.  
XX  
KM Human; cytokine; proteolysis; interferon; IFN; interleukin-10; IL-10;  
KM long-chain cytokine family; short-chain cytokine family; infection;  
KM allergy; heart disease; cancer; liver disorder; autoimmune disease;  
KM growth disorder; diabetes; neurodegenerative disease; antidiabetic;  
KM anti-allergic; cytostatic; immunosuppressive; antidiabetic;  
KM neuroprotective; mutant; mutein.  
XX

```
OS Homo sapiens.
OS Synthetic.
XX MO2004022593-A2.
XX
XX 18-MAR-2004.
XX
XX 08-SEP-2003; 2003MO-IB004347.
XX
XX 09-SEP-2002; 2002US-0409898P.
XX
XX 21-MAR-2003; 2003US-0457135P.
XX
XX (NAUT-) NAUTILUS BIOTECH.
XX
XX Gantler R, Guyon T, Vega M, Driscanti L;
XX WPI; 2004-248447/23.
XX
XX New modified cytokines with increased resistance to proteolysis, useful
XX for diagnosing and treating diseases such as infections, allergies, heart
XX diseases, cancer, liver disorders, autoimmune diseases or diabetes.
XX
XX Disclosure; SEQ ID NO 588; 316pp; English.
XX
XX The invention relates to modified cytokines that exhibit increased
XX resistance to proteolysis compared to unmodified cytokines. The invention
XX also relates to nucleic acid molecules encoding the cytokines, a
XX pharmaceutical composition comprising a nucleic acid molecule in a
XX pharmaceutical carrier, and a method of generating a protein or peptide
XX molecule having a predetermined property or activity, or a pre-selected
XX altered phenotype. The modified cytokine is selected from a member of the
XX interferons (IFNs)/interleukin (IL)-10 protein family, a member of the
XX long-chain cytokine family or a member of the short-chain cytokine
XX family. The composition and method are useful for diagnosing and treating
XX diseases such as infections, allergies, heart diseases, cancer, liver
XX disorders, autoimmune diseases, growth disorders, diabetes or
XX neurodegenerative diseases. This sequence represents a human modified
XX cytokine protein of the invention.
XX
XX Sequence 115 AA;
SQ

Query Match 58.7%; Score 358; DB 8; Length 115;
Best Local Similarity 62.5%; Pred. No. 2.7e-34;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMNRLVATLTLLSTHRTWLIGDGMIPPTENKQHQLCKEVPQGIPTLKNQTAHG 63
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4 ERTSALVETTLALSTHRTLLANETLRIPVPHKQHQLCTEIRFGIGTLESQTVQG 63
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 64 AVDKLFOFNLSTLKEHIERQKRCAGERRVTKFLDYLOVFLGVINTWTPES 115
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 TVERLFPKNSLTKYIDGQKKCKGERRRNVQFLDYLOEFLGVMTWETWIES 115
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 6
AAP93152
ID AAP93152 standard; protein; 113 AA.
XX
XX AAP93152;
XX
XX 15-MAR-1992 (first entry)
XX
XX Sequence of human interleukin-5 (IL-5).
XX
XX B-cell growth factor; lymphokine; B-cell stimulating factor 2.
XX
XX Homo sapiens.
XX
XX GB2217328-A.
XX
XX 25-OCT-1989.
XX
XX 12-APR-1988; 88GB-00008524.
```

```
XX
XX 12-APR-1988; 88GB-00008524.
XX
XX (BRJ-) BRITISH BIO-TECHN L.
XX
XX
XX Edwards RM;
XX
XX WPI; 1989-311767/43.
XX
XX N-PSDB; AAN91647.
XX
XX Synthetic gene encoding human interleukin-5 - has restriction sites at
XX frequent intervals to facilitate manipulation.
XX
XX Disclosure; Fig 3a; 21pp; English.
XX
XX AAN91647 has restriction sites for HindIII, BspMT, NcoI, SpeI, BspMTI,
XX Apat, XbaI, ClaI, BclI, PstI, BamHI and EcoRI. IL5 acts as a B-
XX cell growth and differentiation factor
XX
XX Sequence 113 AA;
SQ

Query Match 58.5%; Score 357; DB 1; Length 113;
Best Local Similarity 61.9%; Pred. No. 3.5e-34;
Matches 70; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 3 VENPMNRLVATLTLLSTHRTWLIGDGMIPPTENKQHQLCKEVPQGIPTLKNQTAHG 62
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MEIPTSALVETTLALSTHRTLLANETLRIPVPHKQHQLCTEIRFGIGTLESQTVQG 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 63 EAVDKLFOFNLSTLKEHIERQKRCAGERRVTKFLDYLOVFLGVINTWTPES 115
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 TVERLFPKNSLTKYIDGQKKCKGERRRNVQFLDYLOEFLGVMTWETWIES 113
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7
ADL89235
ID ADL89235 standard; protein; 115 AA.
XX
XX ADL89235;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human modified cytokine protein #517.
XX
XX Human; cytokine; proteolysis; interferon; IFN; interleukin-10; IL-10;
XX long-chain cytokine family; short-chain cytokine family; infection;
XX allergy; heart disease; cancer; liver disorder; autoimmune disease;
XX growth disorder; diabetes; neurodegenerative disease; antimicrobial;
XX anti-allergic; cytostatic; immunosuppressive; antidiabetic;
XX neuroprotective; mutant; mutein.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX MO2004022593-A2.
XX
XX 18-MAR-2004.
XX
XX 08-SEP-2003; 2003MO-IB004347.
XX
XX 09-SEP-2002; 2002US-0409898P.
XX
XX 21-MAR-2003; 2003US-0457135P.
XX
XX (NAUT-) NAUTILUS BIOTECH.
XX
XX Gantler R, Guyon T, Vega M, Driscanti L;
XX WPI; 2004-248447/23.
XX
XX New modified cytokines with increased resistance to proteolysis, useful
XX for diagnosing and treating diseases such as infections, allergies, heart
XX diseases, cancer, liver disorders, autoimmune diseases or diabetes.
XX
```

PS Disclosure; SEQ ID NO 569; 316pp; English.

XX The invention relates to modified cytokines that exhibit increased

CC resistance to proteolysis compared to unmodified cytokines. The invention

CC also relates to nucleic acid molecules encoding the cytokines, a

CC pharmaceutical composition comprising a nucleic acid molecule in a

CC pharmaceutical carrier, and a method of generating a protein or peptide

CC molecule having a predetermined property or activity, or a pre-selected

CC altered phenotype. The modified cytokine is selected from a member of the

CC interferons (IFNs)/interleukin (IL)-10 protein family, a member of the

CC long-chain cytokine family or a member of the short-chain cytokine

CC family. The composition and method are useful for diagnosing and treating

CC diseases such as infections, allergies, heart diseases, cancer, liver

CC disorders, autoimmune diseases, growth disorders, diabetes or

CC neurodegenerative diseases. This sequence represents a human modified

CC cytokine protein of the invention.

XX

SQ Sequence 115 AA;

Query Match 58.5%; Score 357; DB 8; Length 115;

Best Local Similarity 62.5%; Pred. No. 3,66-34;

Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMNRLVAETLTLLSTHRTWLTGDNLMIPPTENKKNHOLCIKEVFGIDTLKNQTAHG 63

DB 4 EIPTSALVKETLALSTHRTLLIANETLQIPVPHKNHQLCTBEIFQIGTLESQTVGG 63

QY 64 AVDKLFQNLSTLKEHIEROKKRCAGERRVTKFPLDYQVFLGVINTWTPES 115

DB 64 TVERLFFKNLSLTKYIDGQKKCKGBERRRVNQLDYLOEFLGVNMTWTEIIS 115

RESULT 8

AAO30459 standard; protein; 287 AA.

XX AAO30459;

XX 22-SEP-2003 (first entry)

DE hIL5.36 variant protein.

XX hIL5.36 variant protein.

KM Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;

KW tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;

KM IL5; epitope; human; tetanus toxoid; chimeric; variant; mutant; mutein.

OS Homo sapiens.

OS Unidentified.

OS Chimeric.

XX

FT Key Location/Qualifiers

FT Peptide 1..19

FT Protein /note="Human IL5 leader peptide"

FT 20..287

FT /note="Mature hIL5.36 protein"

FT Region 24..44

FT /note="Tetanus toxoid P30 epitope"

FT 273..287

FT /note="Tetanus toxoid P2 epitope"

XX

XX WO200304244-A2.

XX

XX 22-MAY-2003.

XX

XX 15-NOV-2002; 2002WO-DK000764.

XX

XX 16-NOV-2001; 2001DK-00001702.

PR 16-NOV-2001; 2001US-0331575P.

XX

XX (PHAR-) PHARMEXA AS.

PA (KLVS-) KLYSNER S.

PA (NIEL-) NIELSEN F S.

PA (BRAT/) BRATT T.

PA (VOLD/) VOLDORF B.

PA (MOUR/) MOURITSEN S.

XX

PI Klysner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;

XX WPI; 2003-449558/42.

DR N-PSDB; AAL61295.

XX

PT New immunogenic analogue of a polypeptide protein, useful for preparing a

PT composition for treating inflammatory diseases e.g. arthritis.

XX

PS Claim 20; Page 115-117; 196pp; English.

XX

CC The invention relates to immunogenic analogues of multimeric proteins

CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis

CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic

CC analogues. The immunogenic analogue is useful for preparing a composition

CC for treating inflammatory diseases, e.g., arthritis. It is also used in

CC gene therapy. The present sequence is a fusion construct variant which

CC comprises 2 human interleukin 5 (IL5) monomers joined by a glycine linker

CC and including terminally positioned tetanus toxoid epitopes P30 and P2.

CC This sequence is used to illustrate the method of the invention

XX

SQ Sequence 287 AA;

Query Match 58.5%; Score 357; DB 6; Length 287;

Best Local Similarity 61.9%; Pred. No. 1,36-33;

Matches 70; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 3 VENPMNRLVAETLTLLSTHRTWLTGDNLMIPPTENKKNHOLCIKEVFGIDTLKNQTAHG 62

DB 43 EIPTSALVKETLALSTHRTLLIANETLQIPVPHKNHQLCTBEIFQIGTLESQTVGG 102

QY 63 EAVDKLFQNLSTLKEHIEROKKRCAGERRVTKFPLDYQVFLGVINTWTPES 115

DB 103 TVERLFFKNLSLTKYIDGQKKCKGBERRRVNQLDYLOEFLGVNMTWTEIIS 155

RESULT 9

AAP80279 standard; protein; 112 AA.

XX AAP80279;

AC AAP80279;

XX 25-MAR-2003 (revised)

DT 20-NOV-1990 (first entry)

XX

XX Pleiotropic immune factor (PIF).

XX Pleiotropic immune factor (PIF).

KM Pleiotropic immune factor; PIF; immune system mediator; IgA;

KW immunoglobulin secretion; eosinophil-colony stimulating factor;

KW B-cell differentiation factor.

XX

XX Homo sapiens.

XX EP267779-A.

XX

XX 18-MAY-1988.

XX

XX 10-NOV-1987; 87EP-00309935.

XX

XX 10-NOV-1986; 86US-00928900.

PR 05-JAN-1987; 87US-00000551.

XX

XX (SCHB ) SCHERING BIOTECH CORP.

XX

XX Coffman R, Yokota T, Crute JJ, Lee F, Arai K;

PI WPI; 1988-134622/20.

XX

XX New human pleiotropic immune factor and mutant forms - for stimulating

PT immunoglobulin prodn. and new DNA coding sequences.

PS Claim 4; Page 26; 39pp; English.

XX The peptide has eosinophil colony stimulating factor activity (ECSF)

CC and/or B cell differentiation factor activity. It can be used to

CC stimulate prod. of immunoglobulin, esp. IgA, for treating respiratory

CC and gastrointestinal infections. The protein is produced by recombinant

CC DNA techniques using mRNA from cells showing BCSF activity (ATCC CRL

CC 8179). The cloned DNA can also be engineered to express mutants with

CC improved properties. See also AAP80280. (Updated on 25-MAR-2003 to

CC correct PR field.)

XX

SO Sequence 112 AA;

Query Match 58.4%; Score 356; DB 1; Length 112;

Best Local Similarity 62.5%; Pred. No. 4.7e-34;

Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMNRLVAVETLTLSHRTWILGDNLMIPPEKNKHQLCKEYFGIDTLKNGTANGS 63

DB 1 EIPTSALVETLTALSTHRTLLIANETLRIPVVHNHQLCTEETFGIGLESOTVQGG 60

QY 64 AVDKLFONTSLIKHEIEROKRCAGRRMRYTKFLDYLVQFLGVINTEWTPES 115

DB 61 TVERLFKNLSLIKTYIDGQKKCGERRRNVNOFLDYLOEFLGVNTEWTEIES 112

RESULT 10

AAP81038

ID AAP81038 standard; protein; 115 AA.

XX AAP81038;

XX 25-MAR-2003 (revised)

DT 04-DEC-1990 (first entry)

XX

DE Sequence of human B-cell differentiation factor.

XX

XX Immunodeficiency disease; cancer therapy; interleukin; lymphocyte.

XX

OS Homo sapiens.

XX

PN EP261625-A.

XX

PD 30-MAR-1988.

XX

PF 21-SBP-1987; 87EP-00113774.

XX

XX 20-SBP-1986; 86JP-00223284.

PR 21-SBP-1987; 87JP-00236842.

XX

PA (HONJ/) HONJO T.

XX

PI Honjo T, Taketu K, Severinson B;

XX

DR WPI; 1988-085927/13.

XX

PT Recombinant human B-cell differentiation factor - used for diagnosis or

PT treatment of immunodeficiency diseases, various infections and cancers.

XX

XX Claim 8; Page 17; 5pp; English.

XX

XX BCSF has an approx. molecular weight of 13,149. The BCSF is useful in the

CC diagnosis or treatment of e.g. immunodeficiency diseases which occur due

CC to the deficiency of this factor in a living body and also in the

CC treatment of various infections and cancers. (Updated on 25-MAR-2003 to

CC correct PR field.)

XX

SO Sequence 115 AA;

Query Match 58.4%; Score 356; DB 1; Length 115;

Best Local Similarity 62.5%; Pred. No. 4.7e-34;

Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMNRLVAVETLTLSHRTWILGDNLMIPPEKNKHQLCKEYFGIDTLKNGTANGS 63

DB 4 EIPTSALVETLTALSTHRTLLIANETLRIPVVHNHQLCTEETFGIGLESOTVQGG 63

QY 64 AVDKLFONTSLIKHEIEROKRCAGRRMRYTKFLDYLVQFLGVINTEWTPES 115

DB 64 TVERLFKNLSLIKTYIDGQKKCGERRRNVNOFLDYLOEFLGVNTEWTEIES 115

RESULT 11

AAB45489

ID AAB45489 standard; protein; 115 AA.

XX AAB45489;

AC 26-FEB-2001 (first entry)

DT

XX

DE Human interleukin-5 mature protein SEQ ID NO: 1.

XX

XX Asthma; IL-5; interleukin-5; allergy; cytokine; helminthic infection;

KW cancer; eosinophilia; vaccine; allergic rhinitis.

XX

OS Homo sapiens.

XX

PN WO200065058-A1.

XX

PD 02-NOV-2000.

XX

PF 19-APR-2000; 2000WO-DK000205.

XX

PR 23-APR-1999; 99DK-00000552.

PR 06-MAY-1999; 99US-0132811P.

XX

PA (MEBI-) M & B BIOTECH AS.

XX

PI Klyser S;

XX

DR WPI; 2000-672791/65.

XX

PT Down-regulating interleukin 5 (IL-5) activity in humans by administering

PT IL-5 and/or an IL-5 analogue, useful in the treatment, prophylaxis or

PT amelioration of asthma or other chronic allergic conditions.

XX

PS Claim 19; Page 118; 172pp; English.

XX

XX The present invention is concerned with methods of treating asthma,

CC eosinophilia, allergic rhinitis and other allergic diseases. These

CC involve the use of interleukin-5 (IL-5) analogues and modified IL-5

CC proteins and their coding sequences to down-regulate IL-5 activity and

CC thus reduce eosinophil numbers. The allergic diseases may be treated

CC using autovaccines, nucleic acid vaccines or live vaccines. In addition,

CC it is possible that they may be used in the treatment of cancer and

CC helminthic infections

XX

SO Sequence 115 AA;

Query Match 58.4%; Score 356; DB 3; Length 115;

Best Local Similarity 62.5%; Pred. No. 4.7e-34;

Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMNRLVAVETLTLSHRTWILGDNLMIPPEKNKHQLCKEYFGIDTLKNGTANGS 63

DB 4 EIPTSALVETLTALSTHRTLLIANETLRIPVVHNHQLCTEETFGIGLESOTVQGG 63

QY 64 AVDKLFONTSLIKHEIEROKRCAGRRMRYTKFLDYLVQFLGVINTEWTPES 115

DB 64 TVERLFKNLSLIKTYIDGQKKCGERRRNVNOFLDYLOEFLGVNTEWTEIES 115

RESULT 12

ABG94295

ID ABG94295 standard; protein; 115 AA.

AC	ABG94295;
XX	10-DEC-2002 (first entry)
DT	Human mature interleukin 5 protein.
DE	Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
XX	Cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW	vaccine; infectious disease.
KM	Homo sapiens.
OS	MOZ00256905-A2.
PN	25-JUL-2002.
XX	21-JAN-2002; 2002WO-IB000166.
PD	19-JAN-2001; 2001US-0262379P.
PF	04-MAY-2001; 2001US-0288549P.
PR	05-OCT-2001; 2001US-0326998P.
PR	07-NOV-2001; 2001US-0331045P.
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.
PI	Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Seibel P,
Pt	Plosssek C;
PS	WPI; 2002-627351/67.
XX	Molecular antigen array used in the production of vaccines for infectious diseases.
PT	disclosure; Page 422; 441pp; English.
DR	This invention relates to a novel ordered and repetitive antigen array
CC	used in the production of vaccines for infectious diseases. The invention
CC	also discloses a composition comprising a non-natural molecular scaffold
CC	comprising a core particle selected from a core particle of a non-natural
CC	origin and a core particle of natural origin and an organismer comprising
CC	at least one first attachment site, where the organismer is connected to
CC	the core particle by at least one covalent bond. Also disclosed is an
CC	antigen or antigenic determinant with at least one second attachment
CC	site, where the antigen or antigenic determinant is amyloid beta peptide
CC	(Abeta1-42) or its fragment and where the second attachment site is
CC	selected from an attachment site not naturally occurring with the antigen
CC	or antigenic determinant and an attachment site naturally occurring with
CC	the antigen or antigenic determinant, where the second attachment site is
CC	capable of association through at least one non-peptide bond to the first
CC	scaffold interact through the association to form an ordered and
CC	repetitive antigen array. The invention also comprises a coat proteins
CC	capable of forming a capsid which comprises mutant Obeta coat proteins
CC	having an amino acid sequence selected from five amino acid sequences
CC	fully defined in the specification. The compounds of the invention may
CC	have antitubercular, antiallergic, immunomodulatory, cytostatic,
CC	antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC	immunisation and as a vaccine. The present sequence represents a protein
CC	sequence used to create the compositions of the invention
SQ	Sequence 115 AA;
OY	Query Match 58.4%; Score 356; DB 5; Length 115;
Dd	Best Local Similarity 62.5%; Pred. No. 4, 7e-34;
Matches	70; Conservative 16; Mismatches 26; Indels 0; Gaps 0
4	ENPMNRRLVAETLLTLSTRFTWLIGDGNLITPPENKNNHOLCIKEVFQGITLKNOTANGE 63
4	EIPTSALVKETALLSTRTTLILANETLRIPVPHKNHQLCTEEIFQGGITLESOTVQGS 63
64	AVDKLFQWLSTLIKEHIEROKRCAEBRRRVTKTELDLYOVFGIVNTTWEPES 115
64	TVERIFPKLSLIKRYIDQGCKGERRRVNPFLLIODEFLVNMNTWTIS 115

**RESULT 13**

ABG80607  
ABG80607 standard; protein; 115 AA.

ID  
XX ABG80607;  
XX  
XX  
DT 29-NOV-2002 (first entry)  
XX  
DE Human mature Interleukin 5.  
XX  
XX Molecular antigen array; vaccine; antigen; antimicrobial;  
KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;  
KW graft versus host disease; Igg-mediated allergic reaction; anaphylaxis;  
KW adult respiratory distress syndrome; ARDS; Crohn's disease;  
KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;  
KW Grave's disease; systemic lupus erythematosus; osteoporosis;  
KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;  
KW immunoproliferative disease Lymphadenopathy; Alzheimer's disease;  
KW angiotumproliferative Lymphadenopathy; Immunoblastic Lymphadenopathy;  
KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;  
KW enterokinase; cysteine-containing linker.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200256907-A2.  
PD  
XX 25-JUL-2002.  
XX  
PF 21-JAN-2002; 2002MO-IB000169.  
XX  
PR 19-JAN-2001; 2001US-0262379P.  
PR 04-MAY-2001; 2001US-0288549P.  
PR 05-OCT-2001; 2001US-0326998P.  
PR 07-NOV-2001; 2001US-0331045P.  
XX  
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.  
PA (NOVS ) NOVAARTIS PHARMA AG.  
PA (MAUR/) MAURER P.  
PA (LECH/) LECHNER F.  
PA (ORTM/) ORTMANN R.  
PA (LUEO/) LUEBEND R.  
PA (STAU/) STAUFENBIEL M.  
PA (FREY/) FREY P.  
PI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P,  
PI Renner WA, Bachmann M, Tisssot A, Sebbel P, Plösek C,  
DR WPl; 2002-636514/68.  
XX  
XX  
XX  
PT Molecular antigen array used in the production of vaccines for infectious  
XX diseases.  
XX  
SS Disclosure; Page 399; 418pp; English.

The invention relates to a composition comprising: (a) a non-natural molecular scaffold comprising: (1) a core particle selected from: (1) a core particle of a non-natural origin; and (2) a core particle of natural origin; and (ii) an organiser comprising at least one first attachment site, where the organiser is connected to the core particle by at least one covalent bond; (b) an antigen or antigenic determinant with at least one second attachment site, where the antigen or antigenic determinant is anyloidd beta peptide (Abeta 1-42) or its fragment, and where the second attachment site is selected from: (i) an attachment site not naturally occurring with the antigen or antigenic determinant; and (ii) an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site; and CC where the antigen or antigenic determinant and the scaffold interact CC through the association to form an ordered and repetitive antigen array.  
CC Also included is a process for producing a non-naturally occurring CC ordered and repetitive antigen array. The composition is used in

CC immunisation and as a vaccine for diseases such as influenza, graft  
 CC versus host disease, IGH-mediated allergic reactions, anaphylaxis, adult  
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,  
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,  
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia  
 CC gravis, immunoproliferative disease lymphadenopathy,  
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,  
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,  
 CC osteoporosis and infectious diseases. The present sequence is an antigen  
 CC for use in the array of the invention. The antigen is modified to possess  
 CC a cleavage site (enterokinase or factor Xa) and a cysteine-containing N-  
 CC or C-terminal linker peptide which serves as the attachment point to a  
 CC virus like particle or bacterial protein (the scaffold protein)

XX Sequence 115 AA;

Query Match 58.4%; Score 356; DB 5; Length 115;  
 Best Local Similarity 62.5%; Pred. No. 4.7e-34;  
 Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMRLVAVETTLTSLSTRTWLIGDGNLMIPTPENKNOHLCIKVPOGIDTLKNQTAHGE 63  
 DB 4 EIPTSALVETTLTSLSTRTWLIGDGNLMIPTPENKNOHLCIKVPOGIDTLKNQTAHGE 63  
 4 EIPTSALVETTLTSLSTRTWLIGDGNLMIPTPENKNOHLCIKVPOGIDTLKNQTAHGE 63

QY 64 AVDKLFONTSLIKKHIEROKKRCAGSRWVTKFLDYQLVFLGVINTWTPES 115  
 DB 64 TYERLFKNLSLIKXYIDGQKKCGSRRRVNGFLDYQLGSEFLGVNTWTEIIS 115

RESULT 14

AA030453

ID AA030453 standard; protein; 115 AA.

AC AA030453;

DT 22-SRP-2003 (first entry)

DE Human mature Interleukin 5 (IL5) protein.

KW Multimeric protein; Interleukin 5; IL5; TNFalpha; inflammatory disease;  
 KM tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;  
 XX IL5; human.

OS Homo sapiens.

PN WO2003042244-A2.

PD 22-MAY-2003.

PF 15-NOV-2002; 2002WO-DK000764.

PR 16-NOV-2001; 2001DK-00001702.

PR 16-NOV-2001; 2001US-0331575P.

PA (PHAR-) PHARMEA AS.

PA (KLYS-) KLYSNER S.

PA (NIEL/) NIELSEN F S.

PA (BRAT/) BRATT T.

PA (VOLD/) VOLDORGB B.

PA (MOUR/) MOURITSEN S.

PI Klynsner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;

DR WPI; 2003-449558/42.

PT New immunogenic analogue of a polymeric protein, useful for preparing a

XX composition for treating inflammatory diseases e.g. arthritis.

PS Disclosure; Page 105; 196pp; English.

CC The invention relates to immunogenic analogues of multimeric proteins

CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis

CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic

CC analogues. The immunogenic analogue is useful for preparing a composition  
 CC for treating inflammatory diseases, e.g., arthritis. It is also used in  
 CC gene therapy. The present sequence is human mature IL5 protein. This  
 CC sequence is used to illustrate the method of the invention

XX Sequence 115 AA;

Query Match 58.4%; Score 356; DB 6; Length 115;  
 Best Local Similarity 62.5%; Pred. No. 4.7e-34;  
 Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMRLVAVETTLTSLSTRTWLIGDGNLMIPTPENKNOHLCIKVPOGIDTLKNQTAHGE 63  
 DB 4 EIPTSALVETTLTSLSTRTWLIGDGNLMIPTPENKNOHLCIKVPOGIDTLKNQTAHGE 63  
 4 EIPTSALVETTLTSLSTRTWLIGDGNLMIPTPENKNOHLCIKVPOGIDTLKNQTAHGE 63

QY 64 AVDKLFONTSLIKKHIEROKKRCAGSRWVTKFLDYQLVFLGVINTWTPES 115  
 DB 64 TYERLFKNLSLIKXYIDGQKKCGSRRRVNGFLDYQLGSEFLGVNTWTEIIS 115

RESULT 15

ADK17208

ID ADK17208 standard; protein; 115 AA.

AC ADK17208;

DT 06-MAY-2004 (first entry)

DE Human Interleukin-5 processed for repetitive antigen array.

KW anti-allergic; antiasthmatic; cytostatic; vaccine; virus-like particle;  
 KM Interleukin; IL-5; IL-13; ectaxin; repetitive antigen array;  
 XX allergic eosinophilic disease; asthma; Hodgkin's lymphoma.

OS Homo sapiens.

PN WO2003040164-A2.

PD 15-MAY-2003.

PF 07-NOV-2002; 2002WO-EP012455.

PR 07-NOV-2001; 2001US-0331045P.

PR 18-JAN-2002; 2002US-00050902.

PR 21-JUN-2002; 2002WO-IB000166.

PR 19-JUL-2002; 2002US-0396636P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI Bachmann M, Jennings G, Sonderregger I;

DR WPI; 2003-441518/41.

PT Composition comprising an ordered and repetitive antigen or antigenic

PT determinant array, useful as a medicament, or for manufacturing a

PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or

PT Hodgkin's lymphoma.

PS Disclosure; SEQ ID NO 234; 245pp; English.

XX The invention relates to a composition comprising a virus-like particle

XX and at least one antigen, which is a protein or peptide of interleukin

XX (IL)-5, IL-13 or ectaxin and is bound to the virus-like particle, or a

XX core particle with at least one first attachment site and at least one

XX antigen with at least one second attachment site, where the antigen is a

XX protein or peptide of IL-5, IL-13 or ectaxin. The second attachment site

XX is an attachment site naturally or not naturally occurring with the

XX antigen or antigenic determinant. The second attachment site is capable

XX of association to the first attachment site, and where the antigen or

XX antigenic determinant and the core particle interact through the

XX association to form an ordered and repetitive antigen array. The

XX compositions are useful as medicaments, or for manufacturing a medicament

XX or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or





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## OM protein - protein search, using sw model

Run on: August 4, 2005, 17:01:52 ; Search time 29.0964 Seconds

(Without alignments)  
295.042 Million cell updates/sec

Title: US-10-787-382-10

Perfect score: 610  
Sequence: 1 PAVENNMNRLVAFETLTLST.....FLDYLVGVFGVINTWTPES 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep.\*  
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4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/1aa/PCITUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	610	100.0	115	4	US-09-322-409-86
2	610	100.0	115	4	US-09-451-527-86
3	610	100.0	134	4	US-09-332-409-81
4	610	100.0	134	4	US-09-451-527-81
5	601	98.5	134	4	US-09-371-615A-2
6	356	58.4	115	4	US-09-556-818-1
7	356	58.4	134	1	US-08-284-393B-13
8	356	58.4	134	3	US-08-759-628-9
9	356	58.4	134	4	US-09-371-615A-7
10	356	58.4	134	4	US-09-462-941-12
11	356	58.4	134	5	PCT-US95-08950-13
12	356	58.4	134	6	5324640-2
13	356	58.4	134	6	5324640-2
14	351	57.5	121	4	US-09-180-864-2
15	347	56.9	133	4	US-09-371-615A-8
16	347	55.6	126	4	US-09-556-818-6
17	335	54.9	132	4	US-09-556-818-10
18	332.5	54.5	126	4	US-09-556-818-2
19	332.5	54.5	126	4	US-09-556-818-28
20	331.5	54.3	132	4	US-09-556-818-40
21	330.5	54.2	124	4	US-09-556-818-4
22	330.5	54.2	124	4	US-09-556-818-34
23	329.5	54.0	132	4	US-09-556-818-7
24	328.5	53.9	130	4	US-09-556-818-9
25	328.5	53.9	130	4	US-09-556-818-22
26	324	53.1	147	4	US-09-556-818-44
27	322.5	52.9	130	4	US-09-556-818-42

28.	321.5	52.7	124	4	US-09-556-818-5	Sequence 5, Appli
29	321.5	52.7	124	4	US-09-556-818-38	Sequence 38, Appli
30	321	52.6	124	4	US-09-556-818-17	Sequence 17, Appli
31	319.5	52.4	124	4	US-09-556-818-46	Sequence 46, Appli
32	318.5	52.2	130	4	US-09-556-818-56	Sequence 56, Appli
33	317	52.0	113	4	US-09-556-818-12	Sequence 12, Appli
34	317	52.0	110	4	US-09-556-818-21	Sequence 21, Appli
35	315.5	51.7	128	4	US-09-556-818-50	Sequence 50, Appli
36	311	51.0	145	4	US-09-556-818-60	Sequence 60, Appli
37	309.5	50.7	128	4	US-09-556-818-58	Sequence 58, Appli
38	308.5	50.6	122	4	US-09-556-818-54	Sequence 54, Appli
39	301.5	49.4	118	4	US-09-556-818-3	Sequence 3, Appli
40	301.5	49.4	118	4	US-09-556-818-36	Sequence 36, Appli
41	300.5	49.3	141	4	US-09-556-818-11	Sequence 11, Appli
42	299.5	49.1	124	4	US-09-556-818-8	Sequence 8, Appli
43	299.5	49.1	124	4	US-09-556-818-30	Sequence 30, Appli
44	293.5	48.1	124	4	US-09-556-818-13	Sequence 13, Appli
45	291.5	47.8	122	4	US-09-556-818-15	Sequence 15, Appli
46	290.5	47.6	130	4	US-09-556-818-18	Sequence 18, Appli
47	289.5	47.5	116	4	US-09-556-818-52	Sequence 52, Appli
48	289.5	47.5	128	4	US-09-556-818-20	Sequence 20, Appli
49	287.5	47.1	122	4	US-09-556-818-48	Sequence 48, Appli
50	282.5	46.3	122	4	US-09-556-818-16	Sequence 16, Appli
51	282.5	46.3	139	4	US-09-556-818-22	Sequence 22, Appli
52	263.5	43.2	116	4	US-09-556-818-14	Sequence 14, Appli
53	261.5	42.9	132	4	US-09-556-818-19	Sequence 19, Appli
54	72.5	11.9	686	4	US-09-914-259-33	Sequence 33, Appli
55	72	11.8	15	5	PCT-US94-06655-4	Sequence 4, Appli
56	71.5	11.7	683	4	US-09-270-767-46792	Sequence 46792, A
57	71	11.6	323	4	US-09-134-000C-5535	Sequence 5535, Ap
58	69.5	11.4	976	3	US-08-560-005-2	Sequence 2, Appli
59	69.5	11.4	976	3	US-09-195-868-14	Sequence 14, Appli
60	69.5	11.4	976	3	US-09-418-540-2	Sequence 2, Appli
61	69.5	11.4	976	4	US-09-969-528-8	Sequence 2, Appli
62	69.5	11.4	1187	3	US-08-664-962B-8	Sequence 8, Appli
63	69.5	11.4	1187	3	US-09-311-743-3	Sequence 8, Appli
64	69.5	11.4	1189	3	US-09-195-868-15	Sequence 15, Appli
65	69.5	11.4	1239	3	US-09-195-868-28	Sequence 28, Appli
66	68.5	11.2	517	4	US-09-248-796A-14631	Sequence 14631, A
67	68	11.1	466	4	US-09-902-540-13016	Sequence 13016, A
68	67.5	11.1	968	1	US-08-434-730-14	Sequence 14, Appli
69	67.5	11.1	1185	3	US-08-664-962B-2	Sequence 2, Appli
70	67.5	11.1	1185	3	US-09-311-743-2	Sequence 2, Appli
71	67	11.0	2311	3	US-08-934-386-9	Sequence 9, Appli
72	66.5	10.9	312	4	US-09-107-532A-6369	Sequence 6369, Ap
73	66.5	10.9	359	4	US-09-543-681A-4194	Sequence 4194, Ap
74	66	10.8	257	4	US-09-248-796A-14638	Sequence 14638, A
75	66	10.8	604	4	US-09-902-540-10284	Sequence 10284, A
76	66	10.8	2325	3	US-08-417-089-6	Sequence 6, Appli
77	66	10.8	2325	3	US-08-695-651-6	Sequence 6, Appli
78	66	10.8	2325	3	US-08-930-285-6	Sequence 6, Appli
79	66	10.8	2325	3	US-08-695-421-6	Sequence 6, Appli
80	66	10.8	2325	3	US-08-697-826A-10	Sequence 10, Appli
81	65.5	10.7	248	4	US-09-367-293-5	Sequence 5, Appli
82	65	10.7	177	4	US-09-851-873-41	Sequence 41, Appli
83	65	10.7	300	4	US-09-328-352-6714	Sequence 6714, Ap
84	65	10.7	738	4	US-09-538-092-575	Sequence 575, App
85	65	10.7	841	4	US-09-270-767-42870	Sequence 2805, Ap
86	64.5	10.6	172	4	US-09-583-110-2805	Sequence 2805, Ap
87	64.5	10.6	186	4	US-09-107-532A-6672	Sequence 6672, Ap
88	64.5	10.6	205	4	US-09-107-433-3118	Sequence 3118, Ap
89	64.5	10.6	364	4	US-09-252-991A-18473	Sequence 18473, A
90	64.5	10.6	414	4	US-10-067-443-2	Sequence 2, Appli
91	64.5	10.6	439	4	US-10-067-443-19	Sequence 19, Appli
92	64.5	10.6	499	4	US-09-248-796A-19030	Sequence 19030, A
93	64.5	10.6	984	4	US-09-328-352-6926	Sequence 6926, Ap
94	64	10.5	260	4	US-09-107-532A-5350	Sequence 5350, Ap
95	64	10.5	283	4	US-09-540-236-3710	Sequence 3710, Ap
96	63.5	10.4	116	4	US-09-513-999C-4105	Sequence 4105, Ap
97	63.5	10.4	448	2	US-08-878-989-2	Sequence 2, Appli
98	63.5	10.4	448	3	US-09-272-746-2	Sequence 2, Appli
99	63.5	10.4	508	3	US-09-344-700-4	Sequence 4, Appli
100	63.5	10.4	508	4	US-09-563-997A-4	Sequence 4, Appli

## ALIGNMENTS

## RESULT 1

US-09-322-409-86

/ Sequence 86, Application US/09322409  
/ Patent No. 6471957  
/ GENERAL INFORMATION:  
/ APPLICANT: Sim, Gek-Kee  
/ APPLICANT: Yang, Shumin  
/ APPLICANT: Dreitz, Matthew J.  
/ APPLICANT: Wonderling, Ramani S.  
/ TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
/ FILE REFERENCE: IM-2-C1  
/ CURRENT APPLICATION NUMBER: US/09/322,409  
/ CURRENT FILING DATE: 1999-05-28  
/ EARLIER APPLICATION NUMBER: 60/087,306  
/ EARLIER FILING DATE: 1998-05-29  
/ NUMBER OF SEQ ID NOS: 154  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO: 86  
/ LENGTH: 115  
/ TYPE: PRT  
/ ORGANISM: Canis familiaris  
US-09-322-409-86

Query Match 100.0%; Score 610; DB 4; Length 115;

Best Local Similarity 100.0%; Pred. No. 5.4e-71; Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETLTLLSTHRTWLTIGDGNLMIPPENNKHQLCIKVEFGIDTLKNQTA 60  
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Db 1 FAVENPMNRLVAETLTLLSTHRTWLTIGDGNLMIPPENNKHQLCIKVEFGIDTLKNQTA 60

Qy 61 HGEAVDKLFQNLISLKEHIEROKKRCAGSRWVTKFLDYLOVFLGVINTWTPES 115  
|||||  
Db 61 HGEAVDKLFQNLISLKEHIEROKKRCAGSRWVTKFLDYLOVFLGVINTWTPES 115

## RESULT 2

US-09-451-527-86

/ Sequence 86, Application US/09451527  
/ Patent No. 6482403  
/ GENERAL INFORMATION:  
/ APPLICANT: Sim, Gek-Kee  
/ APPLICANT: Yang, Shumin  
/ APPLICANT: Dreitz, Matthew J.  
/ APPLICANT: Wonderling, Ramani S.  
/ TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
/ FILE REFERENCE: IM-2-C2  
/ CURRENT APPLICATION NUMBER: US/09/451,527  
/ CURRENT FILING DATE: 1999-12-01  
/ EARLIER APPLICATION NUMBER: 09/322,409  
/ EARLIER FILING DATE: 1999-05-28  
/ EARLIER APPLICATION NUMBER: 60/087,306  
/ EARLIER FILING DATE: 1998-05-29  
/ NUMBER OF SEQ ID NOS: 174  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO: 86  
/ LENGTH: 115  
/ TYPE: PRT  
/ ORGANISM: Canis familiaris  
US-09-451-527-86

Query Match 100.0%; Score 610; DB 4; Length 115;

Best Local Similarity 100.0%; Pred. No. 5.4e-71; Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETLTLLSTHRTWLTIGDGNLMIPPENNKHQLCIKVEFGIDTLKNQTA 60

Db 1 FAVENPMNRLVAETLTLLSTHRTWLTIGDGNLMIPPENNKHQLCIKVEFGIDTLKNQTA 60  
|||||

Qy 61 HGEAVDKLFQNLISLKEHIEROKKRCAGSRWVTKFLDYLOVFLGVINTWTPES 115  
|||||  
Db 61 HGEAVDKLFQNLISLKEHIEROKKRCAGSRWVTKFLDYLOVFLGVINTWTPES 115

## RESULT 3

US-09-322-409-81

/ Sequence 81, Application US/09322409  
/ Patent No. 6471957  
/ GENERAL INFORMATION:  
/ APPLICANT: Sim, Gek-Kee  
/ APPLICANT: Yang, Shumin  
/ APPLICANT: Dreitz, Matthew J.  
/ APPLICANT: Wonderling, Ramani S.  
/ TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
/ FILE REFERENCE: IM-2-C1  
/ CURRENT APPLICATION NUMBER: US/09/322,409  
/ CURRENT FILING DATE: 1999-05-28  
/ EARLIER APPLICATION NUMBER: 60/087,306  
/ EARLIER FILING DATE: 1998-05-29  
/ NUMBER OF SEQ ID NOS: 154  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO: 81  
/ LENGTH: 134  
/ TYPE: PRT  
/ ORGANISM: Canis familiaris  
US-09-322-409-81

Query Match 100.0%; Score 610; DB 4; Length 134;

Best Local Similarity 100.0%; Pred. No. 6.8e-71; Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETLTLLSTHRTWLTIGDGNLMIPPENNKHQLCIKVEFGIDTLKNQTA 60  
|||||  
Db 20 FAVENPMNRLVAETLTLLSTHRTWLTIGDGNLMIPPENNKHQLCIKVEFGIDTLKNQTA 79

Qy 61 HGEAVDKLFQNLISLKEHIEROKKRCAGSRWVTKFLDYLOVFLGVINTWTPES 115  
|||||  
Db 80 HGEAVDKLFQNLISLKEHIEROKKRCAGSRWVTKFLDYLOVFLGVINTWTPES 134

## RESULT 4

US-09-451-527-81

/ Sequence 81, Application US/09451527  
/ Patent No. 6482403  
/ GENERAL INFORMATION:  
/ APPLICANT: Sim, Gek-Kee  
/ APPLICANT: Yang, Shumin  
/ APPLICANT: Dreitz, Matthew J.  
/ APPLICANT: Wonderling, Ramani S.  
/ TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
/ FILE REFERENCE: IM-2-C2  
/ CURRENT APPLICATION NUMBER: US/09/451,527  
/ CURRENT FILING DATE: 1999-12-01  
/ EARLIER APPLICATION NUMBER: 09/322,409  
/ EARLIER FILING DATE: 1999-05-28  
/ EARLIER APPLICATION NUMBER: 60/087,306  
/ EARLIER FILING DATE: 1998-05-29  
/ NUMBER OF SEQ ID NOS: 174  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO: 81  
/ LENGTH: 134  
/ TYPE: PRT  
/ ORGANISM: Canis familiaris  
US-09-451-527-81

Query Match 100.0%; Score 610; DB 4; Length 134;

Best Local Similarity 100.0%; Pred. No. 6.8e-71;

Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPMNRVAVETLLSTHRTWLIGDGNLMIPTPENKNHOLCIKEVFGIDITLKNQTA 60  
|||  
Db 20 FAVENPMNRVAVETLLSTHRTWLIGDGNLMIPTPENKNHOLCIKEVFGIDITLKNQTA 79  
|||

QY 61 HGRAVDKLFONLSLKEHIEROKKRCGGERWRVTKFLDYLOVFLGVINTEWTPES 115  
|||  
Db 80 HGRAVDKLFONLSLKEHIEROKKRCGGERWRVTKFLDYLOVFLGVINTEWTPES 134  
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RESULT 5  
US-09-371-615A-2  
; Sequence 2, Application US/09371615A  
; Patent No. 6537781  
; GENERAL INFORMATION:  
; APPLICANT: IDEXX LABORATORIES  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING  
; FILE REFERENCE: 03604001700US00  
; CURRENT APPLICATION NUMBER: US/09/371,615A  
; CURRENT FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-09-371-615A-2

Query Match 98.5%; Score 601; DB 4; Length 134;  
Best Local Similarity 99.1%; Pred. No. 9.9e-70;  
Matches 114; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAVENPMNRVAVETLLSTHRTWLIGDGNLMIPTPENKNHOLCIKEVFGIDITLKNQTA 60  
|||  
Db 20 FAVENPMNRVAVETLLSTHRTWLIGDGNLMIPTPENKNHOLCIKEVFGIDITLKNQTA 79  
|||

QY 61 HGRAVDKLFONLSLKEHIEROKKRCGGERWRVTKFLDYLOVFLGVINTEWTPES 115  
|||  
Db 80 HGRAVDKLFONLSLKEHIEROKKRCGGERWRVTKFLDYLOVFLGVINTEWTPES 134  
|||

RESULT 6  
US-09-556-818-1  
; Sequence 1, Application US/09556818  
; Patent No. 6746669  
; GENERAL INFORMATION:  
; APPLICANT: Klyseer, Steen  
; TITLE OF INVENTION: Method For Down-Regulating IL5 Activity  
; FILE REFERENCE: 0459-0428P  
; CURRENT APPLICATION NUMBER: US/09/556,818  
; CURRENT FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 115  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DISULFID  
; LOCATION: (44)  
; OTHER INFORMATION: Interchain disulphide bond to Cys-86 in SEQ ID  
; NAME/KEY: DISULFID  
; LOCATION: (86)  
; OTHER INFORMATION: Interchain disulphide bond to Cys-44 in SEQ ID  
; OTHER INFORMATION: NO:1  
US-09-556-818-1

Query Match 58.4%; Score 356; DB 4; Length 115;  
Best Local Similarity 62.5%; Pred. No. 4e-38;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMNRVAVETLLSTHRTWLIGDGNLMIPTPENKNHOLCIKEVFGIDITLKNQTAHGE 63  
|||  
Db 4 EFTSALVAVETLLSTHRTWLIGDGNLMIPTPENKNHOLCIKEVFGIDITLKNQTAHGE 63  
|||

QY 64 AVDKLFONLSLKEHIEROKKRCGGERWRVTKFLDYLOVFLGVINTEWTPES 115  
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Db 64 TVERLKFONLSLKEHIEROKKRCGGERWRVTKFLDYLOVFLGVINTEWTPES 115  
|||

RESULT 7  
US-08-284-393B-13  
; Sequence 13, Application US/08284393B  
; Patent No. 5696234  
; GENERAL INFORMATION:  
; APPLICANT: Zurawski, Sandra M.  
; TITLE OF INVENTION: MUTINS OF MAMMALIAN CYTOKINES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/284,393B  
; FILING DATE: 01-AUG-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0389  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 134 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-284-393B-13

Query Match 58.4%; Score 356; DB 1; Length 134;  
Best Local Similarity 62.5%; Pred. No. 5e-38;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMNRVAVETLLSTHRTWLIGDGNLMIPTPENKNHOLCIKEVFGIDITLKNQTAHGE 63  
|||  
Db 23 EFTSALVAVETLLSTHRTWLIGDGNLMIPTPENKNHOLCIKEVFGIDITLKNQTAHGE 82  
|||

QY 64 AVDKLFONLSLKEHIEROKKRCGGERWRVTKFLDYLOVFLGVINTEWTPES 115  
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Db 83 TVERLKFONLSLKEHIEROKKRCGGERWRVTKFLDYLOVFLGVINTEWTPES 134  
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RESULT 8  
US-08-759-628-9  
; Sequence 9, Application US/08759628  
; Patent No. 6225446  
; GENERAL INFORMATION:  
; APPLICANT: Altman, Scott W.  
; APPLICANT: Rock, Fernando L.  
; APPLICANT: Bazan, J. Fernando  
; APPLICANT: Kaestlein, Robert A.

TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/759,628  
FILING DATE: 05-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,574  
FILING DATE: 06-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX05520  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 134 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 20..134  
OTHER INFORMATION: /note= "Peptide of Figure 1"  
US-08-759-628-9

Query Match 58.4%; Score 356; DB 3; Length 134;  
Best Local Similarity 62.5%; Pred. No. 5e-38;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMNRVAVETTLSTHRTWLTIGDGNLMIPTPENKNHQLCTKEVFGIDTLKNOTAHGE 63  
DB 23 EIPTSALVETTLALSTHRTLILANETLRIPVPHKNHQLCTKEIFOGIGTLESQTVQGG 82

QY 64 AVDKLFONLSLKEHIEROKRCAGERRVTKFLDYLOVFLGVINTEWTPES 115  
DB 83 TVERLFKNLSLTKYIDGKKCGERRRVNQLDYLOEFLGVMTWTEWIES 134

RESULT 9  
US-09-371-615A-7  
Sequence 7, Application US/09371615A  
Patent No. 6537781  
GENERAL INFORMATION:  
APPLICANT: IDEXX LABORATORIES  
TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING  
FILE REFERENCE: 03604001700US00  
CURRENT APPLICATION NUMBER: US/09/371,615A  
CURRENT FILING DATE: 1999-08-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 7  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Interleukin 5

US-09-371-615A-7  
Query Match 58.4%; Score 356; DB 4; Length 134;  
Best Local Similarity 62.5%; Pred. No. 5e-38;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMNRVAVETTLSTHRTWLTIGDGNLMIPTPENKNHQLCTKEVFGIDTLKNOTAHGE 63  
DB 23 EIPTSALVETTLALSTHRTLILANETLRIPVPHKNHQLCTKEIFOGIGTLESQTVQGG 82

QY 64 AVDKLFONLSLKEHIEROKRCAGERRVTKFLDYLOVFLGVINTEWTPES 115  
DB 83 TVERLFKNLSLTKYIDGKKCGERRRVNQLDYLOEFLGVMTWTEWIES 134

RESULT 10  
US-09-462-941-12  
Sequence 12, Application US/09462941  
Patent No. 6608183  
GENERAL INFORMATION:  
APPLICANT: Cox III, George N  
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins  
FILE REFERENCE: 4152-1-PUS  
CURRENT APPLICATION NUMBER: US/09/462,941  
CURRENT FILING DATE: 2000-01-14  
PRIOR APPLICATION NUMBER: 60/052,516  
PRIOR FILING DATE: 1997-07-14  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-462-941-12

Query Match 58.4%; Score 356; DB 4; Length 134;  
Best Local Similarity 62.5%; Pred. No. 5e-38;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMNRVAVETTLSTHRTWLTIGDGNLMIPTPENKNHQLCTKEVFGIDTLKNOTAHGE 63  
DB 23 EIPTSALVETTLALSTHRTLILANETLRIPVPHKNHQLCTKEIFOGIGTLESQTVQGG 82

QY 64 AVDKLFONLSLKEHIEROKRCAGERRVTKFLDYLOVFLGVINTEWTPES 115  
DB 83 TVERLFKNLSLTKYIDGKKCGERRRVNQLDYLOEFLGVMTWTEWIES 134

RESULT 11  
PCT-US95-08950-13  
Sequence 13, Application PCT/TU89508950  
GENERAL INFORMATION:  
APPLICANT: Zurawski, Sandra M.  
TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08950  
FILING DATE:  
CLASSIFICATION:



Matches	66;	Conservative	18;	Mismatches	29;	Indels	0;	Gaps	0;
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Qy	62	GEAVDKLPQNLSTIK	EHIERQ	KKRC	AGERN	RYTK	FLDY	QVFL	GVINTWTPR 114
Db	80	GGTVEMLPQNLSTIK	KYIDRQ	KEKCG	EBRR	RTNQ	FLDY	QVFL	GVMTSWAME 132

Search completed: August 4, 2005, 17:13:06  
Job time : 29.0964 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 4, 2005, 17:11:16 ; Search time 97.916 Seconds  
(without alignments)  
458.533 Million cell updates/sec

Title: US-10-787-382-10  
Perfect score: 610  
Sequence: 1 FAVENPMNRLVAETLTLST.....FLDYQLGVFLGVINTWTPES 115

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 1752860

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA:\*  
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22: /cgn2\_6/prodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	610	100.0	115	14	US-10-218-654-86
3	610	100.0	115	14	US-10-262-439-86
4	610	100.0	115	16	US-10-787-382-10
5	610	100.0	134	9	US-09-755-633-5
6	610	100.0	134	14	US-10-218-654-81
7	610	100.0	134	14	US-10-262-439-81
8	610	100.0	134	16	US-10-787-382-5
9	358	58.7	115	16	US-10-658-834A-568
10	357	58.5	115	16	US-10-658-834A-569
11	357	58.5	287	14	US-10-295-074-13

12	357	58.5	287	16	US-10-846-911-13	Sequence 13, App1
13	356	58.4	115	14	US-10-289-454-234	Sequence 234, App
14	356	58.4	115	14	US-10-050-902-234	Sequence 234, App
15	356	58.4	115	14	US-10-050-898-234	Sequence 234, App
16	356	58.4	115	14	US-10-295-074-1	Sequence 1, App1
17	356	58.4	115	16	US-10-658-834A-208	Sequence 208, App
18	356	58.4	115	16	US-10-658-834A-574	Sequence 574, App
19	356	58.4	115	16	US-10-658-834A-580	Sequence 580, App
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21	356	58.4	115	16	US-10-658-834A-589	Sequence 589, App
22	356	58.4	115	16	US-10-658-834A-595	Sequence 595, App
23	356	58.4	115	17	US-10-846-911-1	Sequence 1, App1
24	356	58.4	115	17	US-10-872-198-133	Sequence 133, App
25	356	58.4	133	14	US-10-289-454-337	Sequence 337, App
26	356	58.4	133	14	US-10-050-902-337	Sequence 337, App
27	356	58.4	133	14	US-10-050-898-337	Sequence 337, App
28	356	58.4	134	14	US-10-289-454-233	Sequence 233, App
29	356	58.4	134	14	US-10-400-377-12	Sequence 12, App1
30	356	58.4	134	14	US-10-400-708-12	Sequence 12, App1
31	356	58.4	134	14	US-10-298-148-12	Sequence 12, App1
32	356	58.4	134	14	US-10-050-902-233	Sequence 233, App
33	356	58.4	134	14	US-10-050-898-233	Sequence 233, App
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36	356	58.4	134	16	US-10-773-654-12	Sequence 12, App1
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39	356	58.4	134	17	US-10-685-288-12	Sequence 12, App1
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41	356	58.4	134	17	US-10-773-530-12	Sequence 12, App1
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43	356	58.4	134	18	US-10-880-101A-86	Sequence 86, App1
44	356	58.4	134	18	US-10-880-101A-92	Sequence 90, App1
45	356	58.4	134	18	US-10-880-101A-92	Sequence 92, App1
46	356	58.4	136	14	US-10-289-454-336	Sequence 336, App
47	356	58.4	136	14	US-10-050-902-336	Sequence 336, App
48	356	58.4	136	14	US-10-050-898-336	Sequence 336, App
49	356	58.4	138	14	US-10-289-454-335	Sequence 335, App
50	356	58.4	138	14	US-10-050-902-335	Sequence 335, App
51	356	58.4	138	14	US-10-050-898-335	Sequence 335, App
52	356	58.4	285	14	US-10-295-074-9	Sequence 9, App1
53	356	58.4	285	14	US-10-295-074-11	Sequence 11, App1
54	356	58.4	285	16	US-10-846-911-9	Sequence 9, App1
55	356	58.4	285	16	US-10-846-911-11	Sequence 11, App1
56	356	58.4	287	14	US-10-295-074-15	Sequence 15, App1
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61	355	58.2	115	16	US-10-658-834A-585	Sequence 585, App
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68	353	57.9	115	16	US-10-658-834A-580	Sequence 580, App
69	353	57.9	115	16	US-10-658-834A-598	Sequence 598, App
70	352	57.7	115	16	US-10-658-834A-572	Sequence 572, App
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76	351	57.5	115	16	US-10-658-834A-584	Sequence 584, App
77	351	57.5	115	16	US-10-658-834A-591	Sequence 591, App
78	351	57.5	115	16	US-10-658-834A-592	Sequence 592, App
79	351	57.5	115	16	US-10-658-834A-593	Sequence 593, App
80	351	57.5	115	16	US-10-658-834A-589	Sequence 589, App
81	351	57.5	115	16	US-10-658-834A-590	Sequence 590, App
82	348	57.0	115	16	US-10-658-834A-600	Sequence 600, App
83	348	57.0	115	16	US-10-658-834A-570	Sequence 570, App
84	347	56.9	134	14	US-10-289-454-333	Sequence 333, App

85 347 56.9 134 14 US-10-050-902-333 Sequence 333, App  
86 347 56.9 134 14 US-10-050-898-333 Sequence 333, App  
87 344 56.4 136 14 US-10-289-454-332 Sequence 332, App  
88 344 56.4 136 14 US-10-050-902-332 Sequence 332, App  
89 344 56.4 136 14 US-10-050-898-332 Sequence 332, App  
90 343 56.2 133 14 US-10-289-454-235 Sequence 235, App  
91 343 56.2 133 14 US-10-050-902-235 Sequence 235, App  
92 343 56.2 133 14 US-10-050-898-235 Sequence 235, App  
93 343 56.2 133 14 US-10-658-834A-602 Sequence 602, App  
94 343 56.2 133 14 US-10-289-454-334 Sequence 334, App  
95 343 56.2 133 14 US-10-050-902-334 Sequence 334, App  
96 343 56.2 133 14 US-10-050-898-334 Sequence 334, App  
97 342 56.1 115 16 US-10-658-834A-601 Sequence 601, App  
98 76.5 12.5 230 16 US-10-739-930-10556 Sequence 10556, A  
99 74 12.1 15 9 US-09-755-633-20 Sequence 20, Appl  
100 74 12.1 15 16 US-10-787-382-20 Sequence 20, Appl

## ALIGNMENTS

RESULT 1  
US-09-755-633-10 Application US/09755633  
Patent No. US20020127200A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Shumin  
APPLICANT: McCall, Catherine A.  
APPLICANT: Mober, Eric R.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C1-C1  
CURRENT APPLICATION NUMBER: US/09/755, 633  
CURRENT FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: 09/322, 409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087, 306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 10  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-09-755-633-10  
Query Match 100.0%; Score 610; DB 9; Length 115;  
Best Local Similarity 100.0%; Pred. No. 1.2e-63;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 FAVENPMNRLVAETLLTLLSTHRTWLTIGDNLMIPTPENKNHOLCIKEVFGIDITLKNQTA 60  
Qy 1 FAVENPMNRLVAETLLTLLSTHRTWLTIGDNLMIPTPENKNHOLCIKEVFGIDITLKNQTA 60  
Db 1 FAVENPMNRLVAETLLTLLSTHRTWLTIGDNLMIPTPENKNHOLCIKEVFGIDITLKNQTA 60  
Qy 61 HGEAVDKLPONLSLKEHIEROKRCAGGRWRVTKEFLDYLVFLGVINTWTPES 115  
Db 61 HGEAVDKLPONLSLKEHIEROKRCAGGRWRVTKEFLDYLVFLGVINTWTPES 115  
RESULT 2  
US-10-218-654-86  
Sequence 86, Application US/10218654  
Publication No. US20030099609A1  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Drelitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C1  
CURRENT APPLICATION NUMBER: US/10/218, 654  
CURRENT FILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: US/09/322, 409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087, 306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 86  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-10-218-654-86  
Query Match 100.0%; Score 610; DB 14; Length 115;  
Best Local Similarity 100.0%; Pred. No. 1.2e-63;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3  
US-10-262-439-86  
Sequence 86, Application US/10262439  
Publication No. US20030143196A1  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Drelitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/10/262, 439  
CURRENT FILING DATE: 2002-09-30  
PRIOR APPLICATION NUMBER: US/09/451, 527  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: 09/322, 409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087, 306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 86  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-10-262-439-86

Qy 1 FAVENPMNRLVAETLLTLLSTHRTWLTIGDNLMIPTPENKNHOLCIKEVFGIDITLKNQTA 60  
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Db 61 HGEAVDKLPONLSLKEHIEROKRCAGGRWRVTKEFLDYLVFLGVINTWTPES 115  
RESULT 4  
US-10-787-382-10  
Sequence 10, Application US/10787382  
Publication No. US20040191868A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Shumin  
APPLICANT: McCall, Catherine A.

APPLICANT: Weber, Eric R.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C1-C1  
CURRENT APPLICATION NUMBER: US/10/787,382  
CURRENT FILING DATE: 2004-02-24  
PRIOR APPLICATION NUMBER: US/09/755,633  
PRIOR FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-10-787-382-10

Query Match 100.0%; Score 610; DB 16; Length 115;  
Best Local Similarity 100.0%; Pred. No. 1.2e-63;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPMNRVAVATLTLLSTHRTWLTIGDGNLMIPTPENKNHQLCIKEVFGIDTLKNQTA 60  
DB 1 FAVENPMNRVAVATLTLLSTHRTWLTIGDGNLMIPTPENKNHQLCIKEVFGIDTLKNQTA 60  
QY 61 HGEAVDKLFQNLISLKEHIEROKKRCGGERWRTKFLDYQVPLGVINTEWTPBS 115  
DB 61 HGEAVDKLFQNLISLKEHIEROKKRCGGERWRTKFLDYQVPLGVINTEWTPBS 115

RESULT 5  
US-09-755-633-5  
Sequence 5, Application US/09755633  
Patent No. US20020127200A1  
GENERAL INFORMATION:

APPLICANT: Yang, Shumin  
APPLICANT: McCall, Catherine A.  
APPLICANT: Weber, Eric R.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C1-C1  
CURRENT APPLICATION NUMBER: US/09/755,633  
CURRENT FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-09-755-633-5

Query Match 100.0%; Score 610; DB 9; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1.4e-63;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 20 FAVENPMNRVAVATLTLLSTHRTWLTIGDGNLMIPTPENKNHQLCIKEVFGIDTLKNQTA 79  
QY 61 HGEAVDKLFQNLISLKEHIEROKKRCGGERWRTKFLDYQVPLGVINTEWTPBS 115  
DB 80 HGEAVDKLFQNLISLKEHIEROKKRCGGERWRTKFLDYQVPLGVINTEWTPBS 134

RESULT 6  
US-10-218-654-81

Sequence 81, Application US/10218654  
Publication No. US2003009609A1  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Dreitz, Matthew J.  
APPLICANT: Wondertling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C1  
CURRENT APPLICATION NUMBER: US/10/218,654  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: US/09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 81  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-10-218-654-81

Query Match 100.0%; Score 610; DB 14; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1.4e-63;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPMNRVAVATLTLLSTHRTWLTIGDGNLMIPTPENKNHQLCIKEVFGIDTLKNQTA 60  
DB 20 FAVENPMNRVAVATLTLLSTHRTWLTIGDGNLMIPTPENKNHQLCIKEVFGIDTLKNQTA 79  
QY 61 HGEAVDKLFQNLISLKEHIEROKKRCGGERWRTKFLDYQVPLGVINTEWTPBS 115  
DB 80 HGEAVDKLFQNLISLKEHIEROKKRCGGERWRTKFLDYQVPLGVINTEWTPBS 134

RESULT 7  
US-10-262-439-81  
Sequence 81, Application US/10262439  
Publication No. US20030143196A1  
GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Dreitz, Matthew J.  
APPLICANT: Wondertling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/10/262,439  
CURRENT FILING DATE: 2002-09-30  
PRIOR APPLICATION NUMBER: US/09/451,527  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 81  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-10-262-439-81

Query Match 100.0%; Score 610; DB 14; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1.4e-63;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPMNRVAVATLTLLSTHRTWLTIGDGNLMIPTPENKNHQLCIKEVFGIDTLKNQTA 60  
DB 20 FAVENPMNRVAVATLTLLSTHRTWLTIGDGNLMIPTPENKNHQLCIKEVFGIDTLKNQTA 79

```
QY      61 HGEAVDKLFQNLSIKHEIERQKRCGGERWRVTKFLDYLVQLGVINTWTPES 115
        |||||
Db       80 HGEAVDKLFQNLSIKHEIERQKRCGGERWRVTKFLDYLVQLGVINTWTPES 134
```

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RESULT 8
US-10-787-382-5
/ Sequence 5, Application US/10787382
/ Publication NO. US20040191868A1
/ GENERAL INFORMATION:
/ APPLICANT: Yang, Shumin
/ APPLICANT: McCall, Catherine A.
/ APPLICANT: Weber, Eric R.
/ TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY
/ TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
/ FILER REFERENCE: IM-2-CI-C1
/ CURRENT APPLICATION NUMBER: US/10/787,382
/ CURRENT FILING DATE: 2004-02-24
/ PRIOR APPLICATION NUMBER: US/09/755,633
/ PRIOR FILING DATE: 2001-01-05
/ PRIOR APPLICATION NUMBER: 09/322,409
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/087,306
/ PRIOR FILING DATE: 1998-05-29
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 134
/ TYPE: PRT
/ ORGANISM: Canis familiaris
/ US-10-787-382-5

```

Query Match	100.0%	Score 610	DB 16	Length 134
Best Local Similarity	100.0%	Pred. NC 1.4e-63		
Matches 115	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	1	FAVENPNRRLVAEFTLLTSTHRTWLGDNGLMIPTPENKHOCICKEVFGSIDTLNQA	60
Db	20	FAVENPNRRLVAEFTLLTSTHRTWLGDNGLMIPTPENKHOCICKEVFGSIDTLNQA	79
Qy	61	HGEAVDLTPONTSLIKHIEROKKCGEWRRTKPLDYQVLTGYNINTEWPES	115
Db	80	HGEAVDLTPONTSLIKHIEROKKCGEWRRTKPLDYQVLTGYNINTEWPES	134

RESULT 9  
US-10-658-834A-588  
; Sequence 588, Application US/10658834A  
; Publication No. US20040132977A1

1 TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N

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ORGANISM: Homo sapiens  
US-10-658-834A-588

Query Match 58.7%; Score 358; DB 16; Length 115

Best Local Similarity 62.5%; Pred. NO. 6e-34;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0.

```

QY      4 ENPNARKLVATLTLLSTHRTWILGDGNIPTPEKNKHQCIKEVFGQIGDILKNQPAHGE 63
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      4 EIPPSALVKETALLSTHRTLLIANETLRI PVPVKNHQDCTEEIFQGIQTLSEQTVQGG 63
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Qy      64 AVDKLFQNTSLIKHEIRÖKRCACGERMVTKFLDYQVFLGVINTEWTPES 115
      ||:::||::||::||::||::||::||::||::||::||::||::||
Db      64 TVERLFKNLSLIKRYIDGQKKKCGNERRRVQFLDYQVFLGVNTEWITES 115

```

RESULT 10  
US-10-658-834A-569  
; Sequence 569, Application US/10658834A  
; Publication No. US20040132977A1

```

1  APPLICANT: Ganciet, Rene
2  APPLICANT: Guyon, Thierry
3  APPLICANT: Dirlantel, Lila
4  APPLICANT: Vega, Manuel
5  TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
6  TITLE OF INVENTION: Acid
7  TITLE OF INVENTION: Molecules and Related Applications
8  FILE REFERENCE: 38751-922
9  CURRENT APPLICATION NUMBER: US/10/658,834A
10 CURRENT FILING DATE: 2003-09-08
11 PRIOR APPLICATION NUMBER: 60/457,135
12 PRIOR FILING DATE: 2003-03-21
13 PRIOR APPLICATION NUMBER: 60/409,898
14 PRIOR FILING DATE: 2002-09-09
15 NUMBER OF SEQ ID NOS: 1306
16 SOFTWARE: FastSeq for Windows Version 4.0
17 SEQ ID NO 569
18 LENGTH: 115
19 TYPE: prt
20 ORGANISM: Homo sapiens
21 US-10-658-834A-569

```

Query Match	58.5%	Score 357	DB 16	Length 115
Best Local Similarity	62.5%	Pred. NC. 7.8e-34		
Matches 70	Conservative 16	Mismatches 26	Indels 0	Gaps 0

QY 4 ENPNNRIVATLTLLSTHRWMLGDGNLMPTEBNHQICIEVEGQIGDITLKNQAHG 6  
Db 4 EIPSLAVKETLLASTHRTLLIANETLQRPVPHKHNQICTEIEIFQIGTLESQTVQG 6  
QY 64 ANDKLFQNLISLSEHIEKQKRCAGRMRYTKELDYQFLVGIYNNEMRPES 115  
Db 64 TVRELFFQNLISLKYIDGQKKCKGEEERRNQNCLDYDEFLGVMNEMWIIIS 115

RESULT 11  
US-10-295-074-13  
; Sequence 13, Application US/10295074  
; Publication No. US20030185845A1

```

1  TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
2
3  FILE REFERENCE: P1013D00
4
5  CURRENT APPLICATION NUMBER: US/0/295,074
6
7  CURRENT FILING DATE: 2002-11-15
8
9  NUMBER OF SEQ ID NOS: 60
10
11  SOFTWARE: PatentIn version 3.1
12
13  SEQ ID NO 13

```

**ORGANISM:** Artificial sequence

## ! FEATURES:

OTHER INFORMATION: Two human IL5 monomers joined by diglycine linker and including the emminally positioned P30 and P2 epitopes

US-10-295-074-13

Query Match	Similarity	Score	DB	Length
Best Local	61.9%	Pred. No. 2.6e-33		
Matches	70	Conservative 17	Mismatches 26	Indels 0; Gaps 0

  

Qy	3	VENPNRLVATLLSTHRTWLLGDGWLMTPTRENKHOLCIKEVFOGIDTLKNQYAHG	62
Db	43	LEIFTSALVETLMLSTHRTLLANETLRLIPVPHKHOLCTSEIFQIGLTSQTVQG	102
Qy	63	EAVDKLTQNTSLIKHEIERQKRCGGERWRATYKFLDYQLQVFGVINTETPES	115
Db	103	GTVERLTKNLSLKCYIDGQKKKCGEERRRNQFLDYQELFGVWNTMIIES	155

```

RESULT 12
US-10-846-911-13
; Sequence 13, Application US/10846911
; Publication No. US20040258660A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen
; APPLICANT: NIELSEN, Finn Stausholm
; APPLICANT: BRATT, Tomas
; APPLICANT: VOLDORF, Bjorn
; APPLICANT: MOURITSEN, Soren
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: 674542-2018
; CURRENT APPLICATION NUMBER: US/10/846,911
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: PCT/DK02/00764
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,575
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: PA 2001 01702
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Two human ILS monomers joined by diglycine linker and including
; US-10-846-911-13

```

Query Match	58.5%	Score 357;	DB 16;	Length 267;
Best Local Similarity	61.9%	Pred. No.2.6e-33;		
Matches	70;	Conservative 17;	Mismatches 26;	Indels 0; Gaps 0.
Qy	3 VENNPNRLVATLTLLSTHRTWMLGDGNIAMPTEPNKHOLCIKRVFOGITDKNQYTAG 62			
	:	:	:	:
Dd	43 LEIPTSALVETLTLALSTHRTILLANETFLRIPVPAPHKNHOICTSEIFPGISIGTSQTVOG 102			
	:	:	:	:
Qy	63 EAVDVLTONSLIKKEHIEROKCKRCAGERNRTATKPLDYLOVFPGVINTENTPES 115			
	:	:	:	:
Dd	103 GTVARLFKNLSLIKIKIDGKKKGCEERRRNQAFDDTIOEELGVANNITMIES 155			

RESULT 13  
US-10-289-454-234  
Sequence 234, Application US/10289454  
Publication No. US20030157479A1  
GENERAL INFORMATION:  
APPLICANT: Bachmann, Martin  
APPLICANT: Jennings, Gary  
APPLICANT: Sonderegger, Ivo  
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases  
FILE REFERENCE: 1700.0360001  
CURRENT APPLICATION NUMBER: US/10/289,454  
CURRENT FILING DATE: 2003-02-10  
PRIOR APPLICATION NUMBER: US 60/396,636  
PRIOR FILING DATE: 2002-07-19  
PRIOR APPLICATION NUMBER: PCT/IB02/00166  
PRIOR FILING DATE: 2002-01-21

```

: PRIOR APPLICATION NUMBER: US 10/050,902
: PRIOR FILING DATE: 2002-01-18
: PRIOR APPLICATION NUMBER: US 60/331,045
: PRIOR FILING DATE: 2001-11-07
: NUMBER OF SEQ ID NOS: 386
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 234
:
: LENGTH: 115
:
: TYPE: PRT
:
: ORGANISM: processed human IL-5
:
: US-10-289-454-234

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Query Match      58.4%; Score 356; DB 14; Length 115;
Best Local Similarity 62.5%; Pred. No. 1e-33;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0.

QY      4  ENPNRRVAVETLTIVSTHRTWLLIDGDMIMTPTPENKHQOLCKEKFQSGIDTLKNQTAJGE 63
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4  EIPSLAVKETALLSHTRTILLINMETLRIPVPHKNHQOLCTEETFGSIGTLESSTVGG 63
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      64  AVDTLFQNLSTLKEHIEROKKRCAGEBWRVYKFLDYLOVFGVINTENTPES 115
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      64  TVBELFQNLSTLKKYIDQKKKCKCEBRRNVNPFIDYIOEFGVNTENTIIIS 115
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 14
US-10-050-902-234
: Sequence 234, Application US/10050902
: Publication No. US20030175290A1
GENERAL INFORMATION:
: APPLICANT: Renner, Wolfgang A.
: APPLICANT: Bachmann, Martin
: APPLICANT: Tiesot, Alain
: APPLICANT: Maurer, Patrick
: APPLICANT: Lechner, Franziska
: APPLICANT: Sebbel, Peter
: APPLICANT: Plosser, Christine
: TITLE OF INVENTION: Molecular Antigen Array
: FILE REFERENCE: 1700. 0190004
: CURRENT APPLICATION NUMBER: US/10/050.902
: CURRENT FILING DATE: 2002-01-18
: PRIOR APPLICATION NUMBER: US 60/262,379
: PRIOR FILING DATE: 2001-01-19
: PRIOR APPLICATION NUMBER: US 60/289,549
: PRIOR FILING DATE: 2001-05-04
: PRIOR APPLICATION NUMBER: US 60/326,998
: PRIOR FILING DATE: 2001-10-05
: PRIOR APPLICATION NUMBER: US 60/331,045
: PRIOR FILING DATE: 2001-11-07
: NUMBER OF SEQ ID NOS: 350
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 234
: LENGTH: 115
: TYPE: PR1
ORGANISM: Homo sapiens
US-10-050-902-234

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Query      4  ENPNRRVAETITLSTSTRITWLTIGDNLMTPTPENKNHQLCTKEVFGSIDTLKNQTAFGE 63
            | : | | | | | | | | | : | | | | | | | | | | | | | | | |
Db         4  EIPISALVKETLALLSTHRTLLINLETIRLIPVPHKNHQLCTBEIFQSIGTLESSTVGG 63

Query      64  AVDKLFONLSTLKEHIEROKKRCAGEBWRVYTKFLDYLOVFLGVINTENTPES 115
            | : | | | | | | | | | : | | | | | | | | | | | | | | | |
Db         64  TVERTLFONLSTLKKYIDGQKKKCGEBRRRVNQPLDYLOEFLGVANTENTIES 115

RESULT 15
US-10-050-898-234
: Sequence 234, Application US/10050898

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/ Publication No. US20030175711A1
/ GENERAL INFORMATION:
/ APPLICANT: Renner, Wolfgang A.
/ APPLICANT: Bachmann, Martin
/ APPLICANT: Tisack, Alain
/ APPLICANT: Maurer, Patrick
/ APPLICANT: Lechner, Franziska
/ APPLICANT: Seibel, Peter
/ APPLICANT: Plosek, Christine
/ APPLICANT: Orlmann, Rainer
/ APPLICANT: Staufenbiel, Matthias
/ APPLICANT: Frey, Peter
/ TITLE OF INVENTION: Molecular Antigen Array
/ FILE REFERENCE: 1700.0190005
/ CURRENT APPLICATION NUMBER: US/10/050,898
/ CURRENT FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: US 60/262,379
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: US 60/288,549
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US 60/326,998
/ PRIOR FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: US 60/331,045
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 350
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 234
/ LENGTH: 115
/ TYPE: prt
/ ORGANISM: Homo sapiens
US-10-050-898-234

```

```

Query Match      58.4%; Score 356; DB 14; Length 115;
Best local Similarity 62.5%; Pred. No. 1e-33;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY      4 ENPMRLVARTLTLLSTHRTWLTIGDNLMIPTPENINHOUCIKVEFGIDTLKNOTAHGE 63
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      4 EIPTSALVKEITLALSTHRTLTIANETLRIPVPHKHQCTSEIFQIGTLESQTVQGG 63

QY      64 AYDKLFQNTSLIYKEHIERQKRCAGRWYTKFLDYLVPLGIVINTEWTPES 115
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      64 TVERLPKNTSLIKKYIDQKKCKGSRRRVNOPLDYLOEFLGVMNTEWTPES 115

```

Search completed: August 4, 2005, 17:30:12  
 Job time : 98.9116 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 4, 2005, 16:59:07 / Search time 22.6305 Seconds

(without alignments)  
488.938 Million cell updates/sec

Title: US-10-787-382-10

Perfect score: 610  
Sequence: 1 FAVENPMNRLVARTLLTSLT.....FLDYLVGLGVINTWTPES 115

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	491	80.5	134	2	JCS116
2	386	58.4	134	1	A28477
3	347	56.9	133	1	ICMS5
4	332	54.4	132	1	A48418
5	78.5	12.9	258	2	T47758
6	74.5	12.2	1232	2	B39432
7	73.5	12.0	253	2	T47757
8	73	12.0	1199	2	G69698
9	72.5	11.9	451	2	S33816
10	72.5	11.9	649	2	S33816
11	72.5	11.9	677	2	S33814
12	72.5	11.9	666	2	S33815
13	72	11.8	401	2	S28653
14	71	11.6	216	2	B69498
15	71	11.6	300	2	F84594
16	71	11.6	328	2	F64187
17	71	11.6	446	2	S76228
18	71	11.6	461	2	T38698
19	70	11.5	933	2	A59250
20	69.5	11.4	233	2	C97331
21	69.5	11.4	331	2	G83876
22	69.5	11.4	1188	2	JC4889
23	69	11.3	215	2	F45355
24	69	11.3	346	2	S66958
25	69	11.3	759	2	F64652
26	69	11.3	1871	2	D96698
27	68.5	11.2	1894	2	T02155
28	68.5	11.2	190	2	S23712
29	68.5	11.2	638	2	AE2115

30	68.5	11.2	709	2	T32089	hypothetical prote
31	68.5	11.2	1102	2	S65235	probable membrane
32	68	11.1	215	2	B72854	AcOrt-34 protein -
33	68	11.1	414	2	G84311	hypothetical prote
34	68	11.1	529	2	S35306	phytoene dehydroge
35	68	11.1	767	1	COZPCD	ccl10 start contro
36	68	11.1	1055	2	T10432	DNA-directed RNA p
37	68	11.1	1621	2	A82255	hypothetical prote
38	67.5	11.1	1189	2	JC6118	SH2-containing ino
39	67	11.0	215	2	T41780	AcMNPV orf34 - Bom
40	67	11.0	356	2	S15156	myosin heavy chain
41	67	11.0	570	2	AG1228	DNA polymerase bet
42	67	11.0	2311	2	T06161	acetyl-CoA carboxy
43	66.5	10.9	274	2	T21284	hypothetical prote
44	66.5	10.9	590	2	H71977	hypothetical prote
45	66.5	10.9	757	2	T37844	SCF complex protei
46	66.5	10.8	119	2	G87441	DNA-directed RNA p
47	66	10.8	463	2	T28748	hypothetical prote
48	66	10.8	1625	2	T02921	acetyl-CoA carboxy
49	66	10.8	2325	2	T02235	acetyl-CoA carboxy
50	65.5	10.7	248	2	A46652	glucosamine-6-phos
51	65.5	10.7	368	2	A69774	integrase homolog
52	65.5	10.7	520	2	E71416	hypothetical prote
53	65.5	10.7	2269	2	T28677	thopyry protein -
54	65	10.7	295	2	A69636	glycine-tRNA ligas
55	65	10.7	377	2	AE1991	hypothetical prote
56	65	10.7	664	1	JX0336	succinate dehydrog
57	65	10.7	738	1	S51380	protein kinase STR
58	65	10.7	886	2	AD0831	probable acyl-CoA
59	65	10.7	1460	2	T00095	hypothetical prote
60	65	10.7	1685	2	T02750	acetyl-CoA carboxy
61	64.5	10.6	189	2	D89966	truncated transpos
62	64.5	10.6	220	2	A97953	multidrug efflux p
63	64.5	10.6	225	2	S73585	MG068 homolog D02
64	64.5	10.6	246	2	E95085	transcription regu
65	64.5	10.6	451	1	JC6180	stearyl-CoA 9-des
66	64.5	10.6	1570	2	AC2012	hypothetical prote
67	64	10.5	366	2	F89936	conserved hypochet
68	64	10.5	437	2	S50006	preprotein translo
69	64	10.5	453	2	E83517	conserved hypochet
70	64	10.5	570	2	A11581	DNA polymerase bet
71	64	10.5	588	2	D81302	probable ATP/GTP-b
72	64	10.5	1231	1	NBH0H	complement factor
73	63.5	10.4	380	2	H01912	hypothetical prote
74	63.5	10.4	691	2	H81313	ATP-dependent DNA
75	63.5	10.4	693	2	T15728	hypothetical prote
76	63.5	10.4	1012	2	B90389	conserved hypochet
77	63.5	10.4	1520	2	G69634	glutamate synthase
78	63	10.3	133	2	F90037	hypothetical prote
79	63	10.3	281	2	D86637	protein M09G12.1 f
80	63	10.3	290	2	D86686	hypothetical prote
81	63	10.3	354	2	T35529	anthranilate phosp
82	63	10.3	453	2	E86159	hypothetical prote
83	63	10.3	543	2	T32961	hypothetical prote
84	63	10.3	569	2	D82824	regulator of patho
85	63	10.3	670	2	T32221	hypothetical prote
86	63	10.3	746	2	A40636	ferric enterobacti
87	63	10.3	1250	2	A96586	hypothetical prote
88	63	10.3	2429	1	SJHUA	spectrin alpha cha
89	62.5	10.2	269	1	C69651	poliipoprotein dia
90	62.5	10.2	544	2	T42932	virion tegument pr
91	62.5	10.2	1346	2	A57376	probable regulator
92	62.5	10.2	2178	2	S55805	alpha-toxin - Clo
93	62.5	10.2	2228	2	T14029	variant-specific s
94	62.5	10.2	4930	2	B69679	polypeptide synthet
95	62	10.2	187	2	A81291	probable ATP/GTP-b
96	62	10.2	257	2	B89775	hypothetical prote
97	62	10.2	297	2	AD0800	conserved hypochet
98	62	10.2	305	2	C86745	preprotein translo
99	62	10.2	437	2	JC5115	probable fructose-
100	62	10.2	553	2	G71543	

## ALIGNMENTS

```

RESULT 1
JC5116
Interleukin-5 precursor - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 02-Feb-1997 #sequence, revision 27-Feb-1997 #text_change 09-Jul-2004
C/Accession: JC5116
R/Mertens, B.; Gobright, E.; Seow, H.F.
Gene 176, 273-274, 1996
A/Title: The nucleotide sequence of the bovine interleukin-5-encoding cDNA.
A/Reference number: JC5116; MUID:97075944; PMID:8918267
A/Accession: JC5116
A/Molecule type: mRNA
A/Residues: 1-134 <MR>
A/Cross-references: UNIPROT:P52173; EMBL:Z67872; NID:g1113120; PIDN:CAA91779.1; PID:g111
A/Experimental source: Lymphocytes
C/Comment: This protein plays a role in the eosinophilia associated with parasitic disea
C/Genetics:
A/Gene: IL-5
C/Superfamily: Interleukin-5
C/Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
P/1-19/Domain: signal sequence #status predicted <SIG>
P/20-134/Product: Interleukin-5 #status predicted <MAT>
P/63/Dissulfide bonds: Interchain (to 105) #status predicted
P/76,90/Binding site: carbohydrate (Asn) (covalent) #status predicted
P/105/Dissulfide bonds: Interchain (to 63) #status predicted

Query Match      80.5%; Score 491; DB 2; Length 134;
Best Local Similarity 81.6%; Pred. No. 8e-42;
Matches 93; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

OY      2 AVENPMRLVAETLTLLSTRHWLIGDGNLMIPTPENKNHQLCKEYFGSIDTLKNQTAH 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      21 AVASTMKRLVAETLTLLSTRHWLIGDGNLMIPTPENKNHQLCKEYFGSIDTLKNQTAQ 80
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY      62 GEAVNDKLFOMLSLIKHEIEROKKRCAGERNRVTKFLDYLOVFLGVINTEWTPES 115
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      81 GDVAVKKIFQMLSLIKHEIYDLQKKRCGGERRRVKKQFLDYLOVFLGVINTEWTPES 134
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
A28477
Interleukin-5 precursor - human
N/Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil d
C/Species: Homo sapiens (man)
C/Date: 01-Dec-1989 #sequence, revision 07-Jul-1995 #text_change 09-Jul-2004
C/Accession: A28477; A33883; A26112; A39881; JX0106; SI5775
R/Tanabe, T.; Konishi, M.; Mizuta, T.; Noma, T.; Honjo, T.
J. Biol. Chem. 262, 16580-16584, 1987
A/Title: Molecular cloning and structure of the human interleukin-5 gene.
A/Reference number: A28477; MUID:88059042; PMID:2824500
A/Accession: A28477
A/Molecule type: DNA
A/Residues: 1-134 <TA>
A/Cross-references: UNIPROT:P05113; GB:J03478; NID:g186338; PIDN:AAA74469.1; PID:g386822
R/Campbell, H.D.; Tucker, W.Q.J.; Hort, Y.; Martinson, M.E.; Mayo, G.; Clutterbuck, R.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6629-6633, 1987
A/Title: Molecular cloning, nucleotide sequence, and expression of the gene encoding hum
A/Reference number: A33883; MUID:88016145; PMID:3498940
A/Accession: A33883
A/Molecule type: DNA
A/Residues: 1-134 <CM>
A/Cross-references: GB:J02971; NID:g186340; PIDN:AA98620.1; PID:g386823
R/Kanum, C.; Tanabe, T.; Konishi, M.; Kinashi, T.; Noma, T.; Matsuda, F.; Yaocita, Y.; Ta
Nucleic Acids Res. 14, 9149-9158, 1986
A/Title: Cloning of cDNA for human T-cell replacing factor (interleukin-5) and compariso
A/Reference number: A26112; MUID:87066782; PMID:3024129
A/Accession: A26112
A/Molecule type: mRNA
A/Residues: 1-134 <AZU>
A/Cross-references: GB:X04688; NID:g33833; PIDN:CAA28390.1; PID:g33836

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R/Yokota, T.; Coffman, R.L.; Hagiwara, H.; Rennick, D.M.; Takebe, Y.; Yokota, K.; Gemmel]
de Vries, J.; Lee, F.D.; Aral, N.; Aral, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 7388-7392, 1987
A/Title: Isolation and characterization of lymphokine cDNA clones encoding mouse and huma
A/Reference number: A39881; MUID:88041112; PMID:2823259
A/Accession: A39881
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-134 <YOK>
R/Proudfoot, A.E.I.; Davies, J.G.; Turcatti, G.; Wingfield, P.T.
FEBS Lett. 283, 61-64, 1991
A/Title: Human interleukin-5 expressed in Escherichia coli: assignment of the disulfide b
A/Reference number: SI5775; MUID:91243878; PMID:2037074
A/Accession: SI5775
R/Mintake, Y.; Kodama, S.; Katayama, T.; Adachi, H.; Tanaka, S.; Tsujimoto, M.
J. Biochem. 107, 292-297, 1990
A/Title: Structure of recombinant human interleukin 5 produced by chinese hamster ovary c
A/Reference number: JX0106; MUID:90298686; PMID:2361960
A/Accession: JX0106
C/Genetics:
A/Gene: GDB:IL5
A/Cross-references: GDB:120097; OMIM:147850
A/Map position: 5q31.1-5q31.1
A/Intons: 48/3; 59/3; 102/3
C/Superfamily: Interleukin-5
C/Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
P/1-19/Domain: signal sequence #status predicted <SIG>
P/20-134/Product: Interleukin-5 #status predicted <MAT>
P/22/Binding site: carbohydrate (Thr) (covalent) #status experimental
P/47,90/Binding site: carbohydrate (Asn) (covalent) #status predicted
P/63/Dissulfide bonds: Interchain (to 105) #status experimental
P/105/Dissulfide bonds: Interchain (to 63) #status experimental

Query Match      58.4%; Score 356; DB 1; Length 134;
Best Local Similarity 62.5%; Pred. No. 2.3e-28;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

OY      4 ENPMNLVAETLTLLSTRHWLIGDGNLMIPTPENKNHQLCKEYFGSIDTLKNQTAH 63
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      23 EIPTSALVETLTLLSTRHWLIGDGNLMIPTPENKNHQLCKEYFGSIDTLKNQTAH 82
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY      64 AYDKLFQMLSLIKHEIEROKKRCAGERNRVTKFLDYLOVFLGVINTEWTPES 115
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      83 TVERLFLKMLSLIKHYIDGQKKCGERRRRVKKQFLDYLOVFLGVINTEWTPES 134
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
ICM85
Interleukin-5 precursor - mouse
N/Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil d
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1991 #sequence, revision 30-Sep-1991 #text_change 09-Jul-2004
C/Accession: S00807; A38758; A24898; JG0077; P01012; B39881
R/Campbell, H.D.; Sanderson, C.J.; Wang, Y.; Hort, Y.; Martinson, M.E.; Tucker, W.Q.J.; E
Eur. J. Biochem. 174, 345-352, 1988
A/Title: Isolation, structure and expression of cDNA and genomic clones for murine eosin
n-5.
A/Reference number: S00807; MUID:88254802; PMID:3133208
A/Accession: S00807
A/Molecule type: DNA
A/Residues: 1-133 <CM>
A/Cross-references: UNIPROT:P04401; EMBL:X06271; NID:g52685; PIDN:CAA29607.1; PID:g52686
A/Accession: A38758
A/Molecule type: mRNA
A/Residues: 1-133 <CMA>
A/Cross-references: EMBL:X06270; NID:g52687; PIDN:CAA29606.1; PID:g52688
R/Kinashi, T.; Harada, N.; Severinson, E.; Tanabe, T.; Sideras, P.; Konishi, M.; Azuma, C
Nature 324, 70-73, 1986
A/Title: Cloning of complementary DNA encoding T-cell replacing factor and identity with
A/Reference number: A24898; MUID:87065032; PMID:3024009
A/Accession: A24898
A/Molecule type: mRNA
A/Residues: 1-133 <KIN>

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A/Cross-references: EMBL:X04601; NID:G54898; PIDN:CA28266.1; PID:G54899  
 R:Mizuta, T.R.; Tanabe, T.; Nakahubo, H.; Noma, T.; Honjo, T.  
 Growth Factors 1, 51-57, 1988  
 A>Title: Molecular cloning and structure of the mouse interleukin-5 gene.  
 A/Reference number: J50077; MUID:90180853; PMID:3078564  
 A/Accession: J50077  
 A/Molecule type: DNA  
 A/Residues: 1-133 <MIZ>  
 R:Takahashi, T.; Yamaguchi, N.; Mitra, S.; Yamaguchi, Y.; Suda, T.; Tomimaga, A.; Kikuchi, M.; Immunol. 27, 911-920, 1990  
 A>Title: Structural comparison of murine T-cell (B15.1K12)-derived T-cell-replacing factor  
 A/Reference number: PH0102; MUID:91015093; PMID:2215480  
 A/Accession: PH0102  
 A/Molecule type: protein  
 A/Residues: 21-45 'X', 47 <TAK>  
 R:Yokota, T.; Coffman, R.L.; Haglwa, H.; Rimmick, D.M.; Takebe, Y.; Yokota, K.; Gemmel, de Vries, J.; Lee, F.D.; Araki, N.; Araki, K.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 7388-7392, 1987  
 A>Title: Isolation and characterization of lymphokine cDNA clones encoding mouse and human  
 A/Reference number: A39881; MUID:88041112; PMID:2832259  
 A/Accession: B39881  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-14, 'AA', 15-133 <YOK>  
 C/Genetics:  
 A/Intons: 47/3; 58/3; 101/3  
 C/Superfamily: interleukin-5  
 C/Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-133/Product: interleukin-5 #status predicted <MAT>  
 F:46/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:62/Disulfide bonds: interchain (to 104) #status predicted  
 F:75,89/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:104/Disulfide bonds: interchain (to 62) #status predicted

Query Match 56.9%; Score 347; DB 1; Length 133;  
 Best Local Similarity 58.4%; Pred. No. 1.8e-27;  
 Matches 66; Conservative 18; Mismatches 29; Indels 0; Gaps 0;

QY 2 AVENPNRLVAETTLTSTRTWILGDNLMIPPPKKNHQLCKEYFOGIDTLKNOTAH 61  
 Db 20 AMEIPMSVAVETLQISTRALTSNETMRLPVPTRKHNQLCKIGIFOGIDTLKNOTVR 79

QY 62 GEAVDKLFQNLSTLKEHIEROKKRCGERWRVTKFLDYLPVPGVINTWTPME 114  
 Db 80 GGTVEMLFQNLSTLKYTIIDQKCKGERRRTRQFLDYLPVPGVINTWTPME 132

RESULT 4  
 A48418  
 Interleukin-5 precursor - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: A48418; S37641  
 R:Ueberle, K.; Li, W.O.; Qin, Z.H.; Richter, G.; Raabe, T.; Diamantstein, T.; Blankenstedt, Cytokine 3, 72-81, 1991  
 A>Title: The rat interleukin-5 gene: characterization and expression by retroviral gene  
 A/Reference number: A48418; MUID:91355638; PMID:1653053  
 A/Accession: A48418  
 A/Molecule type: DNA  
 A/Status: preliminary  
 A/Residues: 1-132 <UBE>  
 A/Cross-references: UNIPROT:Q08125; EMBL:X54419; NID:G313254; PIDN:CA38283.1; PID:G3132  
 A/Experimental source: cell line TBS-1  
 A/Note: sequence extracted from NCBI backbone (NCBI:63651, NCBI:63652)  
 C/Superfamily: interleukin-5  
 C/Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell  
 F:1-17/Domain: signal sequence #status predicted <SIG>  
 F:18-132/Product: interleukin-5 #status predicted <MAT>  
 F:45,74,89/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:61/Disulfide bonds: interchain (to 103) #status predicted  
 F:103/Disulfide bonds: interchain (to 61) #status predicted

Query Match 54.4%; Score 332; DB 1; Length 132;  
 Best Local Similarity 56.6%; Pred. No. 5.7e-26;  
 Matches 64; Conservative 18; Mismatches 31; Indels 0; Gaps 0;

QY 2 AVENPNRLVAETTLTSTRTWILGDNLMIPPPKKNHQLCKEYFOGIDTLKNOTAH 61  
 Db 19 AMEIPMSVAVETLQISTRALTSNETMRLPVPTRKHNQLCKIGIFOGIDTLKNOTVR 78

QY 62 GEAVDKLFQNLSTLKEHIEROKKRCGERWRVTKFLDYLPVPGVINTWTPME 114  
 Db 79 GGTVEMLFQNLSTLKYTIIDQKCKGERRRTRQFLDYLPVPGVINTWTPME 131

RESULT 5  
 T47758  
 hypothetical protein F2413.60 - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
 C/Accession: T47758  
 R:Nakamura, G.; Partmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; submitted to the Protein Sequence Database, February 2000  
 A/Reference number: Z24475  
 A/Accession: T47758  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-258 <NTA>  
 A/Cross-references: UNIPROT:Q9M1K0; EMBL:AL138655  
 A/Experimental source: cultivar Columbia; BAC clone F2413  
 C/Genetics:  
 A/Map position: 3  
 A/Intons: 109/3  
 A/Note: F2413.60  
 C/Superfamily: Arabidopsis thaliana hypothetical protein F2413.60

Query Match 12.9%; Score 78.5; DB 2; Length 258;  
 Best Local Similarity 26.8%; Pred. No. 2.4;  
 Matches 22; Conservative 15; Mismatches 38; Indels 7; Gaps 2;

QY 9 RLVAETTLTSTRTWILGDNLMIPPPKKNHQLCKEYFOGIDTLKNOTAH 64  
 Db 161 KAAVNYSTVSATR--LGNENWVQISSKINHPSTISNVLGLEDPRFVLVDWSSRSQ 217

QY 65 VDKLFQNLSTLKEHIEROKKRC 86  
 Db 218 GERLFTLHQLCKEYKLVKNC 239

RESULT 6  
 B39432  
 ATP-dependent deoxyribonuclease chain A adda - Bacillus subtilis  
 N/Alternate names: ATP-dependent exonuclease synthesis protein adda  
 C/Species: Bacillus subtilis  
 C/Date: 21-Feb-1992 #sequence\_revision 21-Feb-1992 #text\_change 09-Jul-2004  
 C/Accession: B39432; H69582  
 R:Kooistra, J.; Venema, G.  
 J. Bacteriol. 173, 3644-3655, 1991  
 A>Title: Cloning, sequencing, and expression of Bacillus subtilis genes involved in ATP-c  
 A/Reference number: A39432; MUID:91267926; PMID:1646786  
 A/Accession: B39432  
 A/Molecule type: DNA  
 A/Status: preliminary  
 A/Residues: 1-1232 <KOO>  
 A/Cross-references: UNIPROT:P23478; GB:M63489; NID:G142438; PIDN:AAA22201.1; PID:G142440  
 R:Kunert, F.; Ogasawara, N.; Moszer, I.; Albrecht, A.M.; Alloni, G.; Azevedo, V.; Bertier  
 C.; Bron, S.; Brouillet, S.; Buschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi  
 A.; Ehrlich, S.D.; Emmerson, P.T.; Eutian, K.D.; Errington, J.; Fabret, C.; Ferrar, E.  
 Nature 390, 249-256, 1997  
 A/Authors: Foulger, D.; Fultz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallec  
 tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holappel, S.; Hosono, S.; Hullo, M.F.;  
 Koester, F.; Koningsveld, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidis, A.; Lardiniois,  
 A/Authors: Lander, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,  
 Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,

A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot, A.; Schuch, M.; Yamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
 A/Authors: Yoshikawa, H.F.; Zumbstein, R.; Yoshikawa, H.; Danchin, A.  
 A/Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
 A/Reference number: A69580; PMID:98044033; PMID:9384377  
 A/Accession: H69582  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-1232 <KUN>  
 A/Cross-references: GB:Z99109; GB:AL009126; NID:g2632260; PIDN:CAB12903.1; PID:AL183065;  
 A/Experimental source: strain 168  
 C/Genetics:  
 A/Gene: addA  
 C/Keywords: nucleotide binding; P-loop  
 F/30-37/Region: nucleotide-binding motif A (P-loop)

Query Match 12.2%; Score 74.5; DB 2; Length 1232;  
 Best Local Similarity 22.2%; Pred. No. 37;  
 Matches 24; Conservative 24; Mismatches 37; Indels 23; Gaps 4;

QY 3 VENNPRVLVATLTLLSTHRTWLG--DGNLMIPTPENKHQLCIKVFGQIDTLKNQTA 60  
 Db 633 IDNPY-----QDPLASVLSRPIVGADENLSLRLENKAPY-----YAMNDYLA 679  
 Matches 24; Conservative 24; Mismatches 37; Indels 23; Gaps 4;

QY 61 HGEAVDCLFQNLISLKEHIERQK-----KRCAGERNVTKFDYL 100  
 Db 680 AGDRSDELYQKNTFYGHLOKMPAFSKNHSVSELIENVYDPTKMDYV 727

RESULT 7  
 T47757  
 hypothetical protein F2413.50 - *Arabidopsis thaliana*  
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

C/Accession: T47757  
 R/Vyakatura, G.; Fattmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;  
 submitted to the Protein Sequence Database, February 2000  
 A/Reference number: Z24475  
 A/Accession: T47757

A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-253 <NTA>  
 A/Cross-references: UNIPROT:Q9MKL1; EMBL:AL138655  
 A/Experimental source: cultivar Columbia; BAC clone F2413

C/Genetics:  
 A/Map position: 3  
 A/Intons: 104/3  
 A/Motif: F2413.50  
 C/Superfamily: *Arabidopsis thaliana* hypothetical protein F2413.60

Query Match 12.0%; Score 73.5; DB 2; Length 253;  
 Best Local Similarity 27.1%; Pred. No. 7.5;  
 Matches 23; Conservative 15; Mismatches 34; Indels 13; Gaps 3;

QY 9 RLVAETLTLLSTHRTWLGIDGNLMIPTPENKHQLCIKVFGQID-----TLKQTAH 61  
 Db 156 KAVASYLSTVSATR---LGDNEVWVQSSSKIHNFISNVLGGIIEGDFLVVSSSRQ 212

QY 62 GEAVDCLFQNLISLKEHIERQKRC 86  
 Db 213 GE---RLFYTLHQVENMDYKINC 234

# RESULT 8

G69698  
 RNA polymerase (beta' subunit) tpoC - *Bacillus subtilis*  
 C/Species: *Bacillus subtilis*  
 C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

C/Accession: G69698  
 R/Kuner, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cinc, A.; Ehrlich, S.D.; Emerson, P.T.; Eutlian, K.D.; Farrington, J.; Fabref, C.; Ferrari, R.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fume, S.; Gallazzi, A.; Gallier, Iech, J.; Harwood, C.R.; Henat, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lamber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Muegel, Y.M.; Ogasawa, K.; Ogawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sedate, Y.; Sato, T.; Scanlon, A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot, A.; Schuch, M.; Yamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
 A/Authors: Yoshikawa, H.F.; Zumbstein, R.; Yoshikawa, H.; Danchin, A.  
 A/Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
 A/Reference number: A69580; PMID:98044033; PMID:9384377  
 A/Accession: H69582  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-1199 <KUN>  
 A/Cross-references: UNIPROT:P37871; GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11884.1  
 A/Experimental source: strain 168  
 C/Genetics:  
 A/Gene: tpoC  
 C/Superfamily: *Bacillus coli* DNA-directed RNA polymerase beta' chain

Query Match 12.0%; Score 73; DB 2; Length 1199;  
 Best Local Similarity 34.7%; Pred. No. 51;  
 Matches 26; Conservative 12; Mismatches 31; Indels 6; Gaps 4;

QY 35 TPEKQKQSLSEKRYAYLDKNGKPKQASMGABRHHLDIDLVKSDMLKSLKTSQSQ 201  
 Db 142 TPEKQKQSLSEKRYAYLDKNGKPKQASMGABRHHLDIDLVKSDMLKSLKTSQSQ 201

QY 90 -RWRVTKFDLYQVF 103  
 Db 202 RRTRAIKRLEVLAEAF 216

RESULT 9  
 S33816  
 kinesin light chain isoform 4 - sea urchin (*Strongylocentrotus purpuratus*)  
 C/Species: *Strongylocentrotus purpuratus* (purple urchin)  
 C/Date: 08-Dec-1993 #sequence\_revision 01-Dec-1995 #text\_change 09-Jul-2004

C/Accession: S33816  
 R/Medman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.  
 J. Mol. Biol. 231, 155-158, 1993  
 A/Title: Sequences of sea urchin kinesin light chain isoforms.  
 A/Reference number: S33813; PMID:93267648; PMID:8496962

A/Accession: S33816  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-451 <MED>  
 A/Cross-references: UNIPROT:Q05090; EMBL:L08258; NID:G161531; PID:G161532

Query Match 11.9%; Score 72.5; DB 2; Length 451;  
 Best Local Similarity 25.9%; Pred. No. 18;  
 Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 27 GGNLMIPTPENKHQLC--IKVFGQIDTLKNQTAHGEAVDCLFQNLISLKEHIERQK 84  
 Db 15 GGNL-----SQBILITGTREVIGKGLQKNE--HNDIINSLYQSLMKLKKDTGDSN 65

QY 85 RCAGERNVTKFDLYQVF 105  
 Db 66 LVEKTDIIEKSLSELDLIG 86

# RESULT 10

S33813  
 kinesin light chain - sea urchin (*Strongylocentrotus purpuratus*)  
 C/Species: *Strongylocentrotus purpuratus* (purple urchin)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004

C/Accession: S33813  
 R/Medman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.  
 J. Mol. Biol. 231, 155-158, 1993

A/Title: Sequences of sea urchin kinesin light chain isoforms.  
A/Reference number: S33813; MUID:93267648; PMID:8496962  
A/Accession: S33813  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-649 <MED>  
A/Cross-references: UNIPROT:Q05090; EMBL:L10233; NID:g161525; PID:g161526

Query Match 11.9%; Score 72.5; DB 2; Length 649;  
Best Local Similarity 25.9%; Pred. No. 28;  
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 27 GDGNLMIPPEKNHOLC--IKVFOGIDTLKQTAHGAVDKLPONTSLIKEHIEROKK 84  
DB 15 GQGNL-----SQEQIITGTRVYIKGLEQKNE--HNDILNSLYSLKMLKKDTPDSN 65  
QY 85 RCAGERNRVTKFLDYQLVPLG 105  
DB 66 LVEKTDIIKSLSLSLGLG 86

## RESULT 11

S33814  
kinesin light chain - sea urchin (Strongylocentrotus purpuratus)  
C/Species: Strongylocentrotus purpuratus (purple urchin)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S33814  
R/Wedman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.  
J. Mol. Biol. 231, 155-158, 1993  
A/Title: Sequences of sea urchin kinesin light chain isoforms.  
A/Reference number: S33813; MUID:93267648; PMID:8496962  
A/Accession: S33814  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-677 <MED>  
A/Cross-references: UNIPROT:Q05090; EMBL:L10234; NID:g161527; PID:g161528

Query Match 11.9%; Score 72.5; DB 2; Length 677;  
Best Local Similarity 25.9%; Pred. No. 30;  
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 27 GDGNLMIPPEKNHOLC--IKVFOGIDTLKQTAHGAVDKLPONTSLIKEHIEROKK 84  
DB 15 GQGNL-----SQEQIITGTRVYIKGLEQKNE--HNDILNSLYSLKMLKKDTPDSN 65  
QY 85 RCAGERNRVTKFLDYQLVPLG 105  
DB 66 LVEKTDIIKSLSLSLGLG 86

## RESULT 12

S33815  
kinesin light chain isoform 3 - sea urchin (Strongylocentrotus purpuratus)  
C/Species: Strongylocentrotus purpuratus (purple urchin)  
C/Date: 08-Dec-1993 #sequence\_revision 01-Dec-1995 #text\_change 09-Jul-2004  
C/Accession: S33815; S36727  
R/Wedman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.  
J. Mol. Biol. 231, 155-158, 1993  
A/Title: Sequences of sea urchin kinesin light chain isoforms.  
A/Reference number: S33813; MUID:93267648; PMID:8496962  
A/Accession: S33815  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-686 <MED>  
A/Cross-references: UNIPROT:Q05090; EMBL:L10235  
R/Wedman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.  
submitted to the EMBL Data Library, February 1993  
A/Reference number: S36727  
A/Accession: S36727  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-568, 'A', 570-686 <MED>  
A/Cross-references: EMBL:L10235; NID:g161529; PID:g161530

Query Match 11.9%; Score 72.5; DB 2; Length 686;  
Best Local Similarity 25.9%; Pred. No. 30;  
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 27 GDGNLMIPPEKNHOLC--IKVFOGIDTLKQTAHGAVDKLPONTSLIKEHIEROKK 84  
DB 15 GQGNL-----SQEQIITGTRVYIKGLEQKNE--HNDILNSLYSLKMLKKDTPDSN 65  
QY 85 RCAGERNRVTKFLDYQLVPLG 105  
DB 66 LVEKTDIIKSLSLSLGLG 86

## RESULT 13

S28653  
hypothetical protein IS (insertion sequence ISM1) - Methanobrevibacter smithii  
C/Species: Methanobrevibacter smithii  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S28653  
R/Hamilton, P.T.; Reeve, J.N.  
Mol. Gen. Genet. 200, 47-59, 1985  
A/Title: Structure of genes and an insertion element in the methane producing archaeobacter  
A/Reference number: S28653; MUID:85295498; PMID:2933814  
A/Accession: S28653  
A/Molecule type: DNA  
A/Residues: 1-401 <HAM>  
A/Cross-references: UNIPROT:P22344; EMBL:X02587; NID:g44519; PIDN:CAA26424.1; PID:g44520  
C/Genetics:  
A/Mobile element: insertion sequence ISM1  
C/Superfamily: Methanobrevibacter smithii hypothetical protein IS (insertion sequence ISM1)

Query Match 11.8%; Score 72; DB 2; Length 401;  
Best Local Similarity 21.7%; Pred. No. 18;  
Matches 23; Conservative 18; Mismatches 33; Indels 32; Gaps 3;

QY 6 PMRLVAETTLTSTRTWMLGDGNLMIPPEKNHOLCIKEVFOGID-----TLKQTA 60  
DB 247 PMRLVAETTLTSTRTWMLGDGNLMIPPEKNHOLCIKEVFOGID-----TLKQTA 60  
QY 61 HGAVDKLPONTSLIKEHIEROKKRCAGERNRVTKFLDYQLVPLG 106  
DB 285 NGKQRHIYENNAQELKNCFRNSKKA-----IEQFYQYQKXTAI 325

## RESULT 14

B69498  
hypothetical protein AF1987 - Archaeoglobus fulgidus  
C/Species: Archaeoglobus fulgidus  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: B69498  
R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A/Authors: Overbeek, R.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.  
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeobacter  
A/Reference number: A69250; MUID:98049343; PMID:9389475  
A/Accession: B69498  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-216 <KLE>  
A/Cross-references: UNIPROT:Q28292; GB:AB000966; GB:AB000782; NID:G2689289; PIDN:AA889271

Query Match 11.6%; Score 71; DB 2; Length 216;  
Best Local Similarity 30.6%; Pred. No. 11;  
Matches 26; Conservative 20; Mismatches 29; Indels 10; Gaps 4;

QY 27 GDGNLMIPPEKNHOLCIKEVFOGIDTLKQTAHGAVDKLPONTSLIKEHIEROKK 85  
DB 119 GDSVIRIPIPP-----IKVNEVDKLEIRALERGGSVDSINKLIELVEGKLEQKCY 171

```

QY      86 CAGERMRVTKFLDYLVQVFLGVINTE 110
      172 MA-QRARMSTYHLNGLEED-GLVYTE 194
Db

```

**RESULT 15**

hypothetical protein At2g20890 [imported] - Arabidopsis thaliana  
C|Species: Arabidopsis thaliana (mouse-ear cress)  
C|Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C|Accession: P84594  
R|Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Meftal, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.;  
Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A|Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A|Reference number: A84420; MUID:20083487; PMID:10617197  
A|Accession: P84594  
A|Status: preliminary  
A|Molecule type: DNA  
A|Residues: 1-300 <STO>  
A|Cross-references: UNIPROT:Q9SKT0; GB:AEO02093; NID:g4454459; PIDN:AA020906.1; GSPDB:GN  
C|Genetics:  
A|Gene: At2g20890  
A|Map position: 2

	Query Match	Similarity	Score	DB	Length	300;
	Best Local	Similarity	31.4%;	Pred. No.	16;	
Matches	27;	Conservative	15;	Mismatches	26;	Indels 18; Gaps 5;
Qy	34	PPEKNHQLCT-----KEYVQGSIDTLKNGCAHGAVDKLFQNLSTLKHIEROKRCA	87			
Db	219	PLVDK---LCSLNLNKKSVDRDIDVTRN-----LISKLVAKELLERIEKKK-Q	268			
Qy	88	GERMRVTFELDYQVFLGVINTETPT	113			
Db	269	GERASQKANEETISKCLG--DTLYNP	292			

Search completed: August 4, 2005, 17:12:00  
Job time : 23.6305 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 4, 2005, 16:50:50 ; Search time 104.378 Seconds  
(without alignments)  
564.193 Million cell updates/sec

Title: US-10-787-382-10

Perfect score: 610  
Sequence: 1 PAVENPMNRVAVETLTLLST.....FLDYLVGLGVNTWTPES 115

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

1: uniprot\_03:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	610	100.0	134 1 IL5 CANFA	Q95J76 canis fami
2	563	92.3	118 2 Q9TV10	Q9TV10 canis fami
3	510	83.6	134 1 IL5 FELCA	Q77515 felis silve
4	501	82.8	134 2 Q9TSD7	Q9TSD7 felis silve
5	505	82.1	134 2 Q9MYM5	Q9MYM5 sus scrofa
6	494	81.0	134 1 IL5 HORSE	Q02639 equus cabal
7	491	80.5	134 1 IL5 BOVIN	P52173 bos taurus
8	487	79.8	132 1 IL5 SHEEP	Q28566 ovis aries
9	382	62.6	134 2 Q8MRH1	Q8MRH1 salmistr bci
10	372	61.0	135 1 IL5 CAVRO	Q08987 cavia porce
11	361	59.2	134 1 IL5 CERTO	P46685 cercopithec
12	358	58.7	132 1 IL5 MERIN	Q62575 meriones un
13	356	58.4	134 1 IL5 HUMAN	P05113 homo sapien
14	354	58.0	132 1 IL5 SIGHT	Q96819 sigmodon hi
15	352	57.7	134 1 IL5 MACMU	P48093 macaca mula
16	347	56.9	133 1 IL5 MOUSE	P04401 mus musculu
17	346	56.7	133 1 IL5 MACRU	Q94191 macropus eu
18	332	54.4	132 1 IL5 RAT	Q08125 rattus norv
19	325	53.3	132 2 Q9R2C9	Q9R2C9 rattus norv
20	214	35.1	48 2 Q6PVS2	Q6PVS2 ovine aries
21	109.5	18.0	40 2 Q9X192	Q9X192 sinthopsis
22	94.5	15.5	590 1 MP44_MYVL	Q9q8q1 myxoma vltu
23	80.5	13.2	452 2 Q7S4A6	Q7S4A6 aabhyra goss
24	78.5	12.9	258 2 Q9MIK0	Q9MIK0 arabidopsis
25	77	12.6	487 2 Q7R8B3	Q7R8B3 plasmodium
26	76.5	12.5	158 2 Q96575	Q96575 leucophaea
27	75	12.3	292 2 Q8RUD3	Q8RUD3 methanosarc
28	75	12.3	360 2 Q62M23	Q62M23 burkholderi
29	74.5	12.3	360 2 Q63S03	Q63S03 burkholderi
30	74.5	12.2	1232 1 ADDA_BACSU	P23478 bacillus su
31	74	12.1	355 2 Q72418	Q72418 listeria mo

32	73.5	12.0	161 2 Q6IL05	Q6IL05 drosophila
33	73.5	12.0	253 2 Q9MIK1	Q9MIK1 arabidopsis
34	73.5	12.0	655 2 Q7MW24	Q7MW24 porphyromon
35	73	12.0	248 2 Q8RVR0	Q8RVR0 helianthus
36	73	12.0	623 2 Q7XRH1	Q7XRH1 oryza sativ
37	73	12.0	661 2 Q921P5	Q921P5 mus musculu
38	73	12.0	1199 1 DHSB_MOUSE	Q8K233 mus musculu
39	73	12.0	1199 1 RPOC_BACSU	P37871 bacillus su
40	72.5	11.9	229 2 Q9CLF5	Q9CLF5 pasteurella
41	72.5	11.9	418 2 Q8S1N1	Q8S1N1 oryza sativ
42	72.5	11.9	510 2 Q8GWT4	Q8GWT4 arabidopsis
43	72.5	11.9	611 2 Q6M0A6	Q6M0A6 methanococc
44	72.5	11.9	645 2 Q8IHQ8	Q8IHQ8 plasmodium
45	72.5	11.9	686 2 KLC_STRPU	Q05090 strongyloce
46	72.5	11.9	296 2 Q8QV4	Q8QV4 methanosarc
47	72	11.8	401 1 Y148_METSM	P22314 methanobrev
48	72	11.8	562 2 Q7TH69	Q7TH69 lycoris pot
49	71.5	11.7	437 1 SECY_STRGB	Q59912 streptomyce
50	71.5	11.7	595 2 Q6CS00	Q6CS00 kluyveromyc
51	71.5	11.7	823 2 Q9X206	Q9X206 drosophila
52	71	11.6	216 2 Y187_ARCFU	Q28292 archaeoglob
53	71	11.6	300 2 Q9SKT0	Q9SKT0 arabidopsis
54	71	11.6	302 2 Q83IU2	Q83IU2 enterococcu
55	71	11.6	328 1 YB70_HARIN	Q57527 haemophilus
56	71	11.6	446 2 P743S0	P743S0 synechocyst
57	71	11.6	461 1 T1P1_SCHPO	P79065 schistosac
58	71	11.6	2321 2 Q947M6	Q947M6 setaria ita
59	70.5	11.6	224 2 Q7PYK6	Q7PYK6 anopheles g
60	70.5	11.6	320 2 Q8TSW7	Q8TSW7 methanosarc
61	70.5	11.6	347 2 Q6N9Z5	Q6N9Z5 rhodospheudo
62	70.5	11.6	480 2 Q61WP4	Q61WP4 brachydanio
63	70.5	11.6	1104 2 Q9PKR7	Q9PKR7 arabidopsis
64	70	11.5	180 1 HSLV_HELHP	Q7V133 helicobacte
65	70	11.5	246 2 Q84ID6	Q84ID6 chrysanthem
66	70	11.5	294 2 Q64UD4	Q64UD4 uncultured
67	70	11.5	313 2 Q8PC22	Q8PC22 xanthomonas
68	70	11.5	340 2 Q6FMT0	Q6FMT0 candida gla
69	70	11.5	406 2 Q9DSQ3	Q9DSQ3 mus musculu
70	70	11.5	437 2 Q8DJY2	Q8DJY2 synechococc
71	70	11.5	533 2 Q7N6A1	Q7N6A1 photorhabdu
72	70	11.5	623 2 Q7Q4J4	Q7Q4J4 anopheles g
73	70	11.5	633 2 Q6BW69	Q6BW69 debaryomyce
74	70	11.5	814 2 Q6FIR9	Q6FIR9 candida gla
75	70	11.5	899 2 Q66RP8	Q66RP8 lolium mult
76	70	11.5	933 2 Q04145	Q04145 acetabulari
77	70	11.5	1103 2 Q7EXB5	Q7EXB5 anopheles g
78	70	11.5	1136 2 Q6XZB5	Q6XZB5 solanum tub
79	70	11.5	1136 2 Q6XZB8	Q6XZB8 solanum tub
80	70	11.5	1136 2 Q6XZB8	Q6XZB8 solanum tub
81	70	11.5	2321 2 Q84T05	Q84T05 setaria ita
82	70	11.5	4189 2 Q6B144	Q6B144 debaryomyce
83	69.5	11.4	120 2 Q9CV87	Q9CV87 mus musculu
84	69.5	11.4	253 2 Q97D65	Q97D65 clostridium
85	69.5	11.4	293 2 Q7XAB8	Q7XAB8 solanum tub
86	69.5	11.4	331 2 Q9KXV9	Q9KXV9 bacillus ha
87	69.5	11.4	454 2 Q9U0X2	Q9U0X2 plasmodium
88	69.5	11.4	676 2 Q7YKY5	Q7YKY5 magania par
89	69.5	11.4	976 2 Q13544	Q13544 homo sapien
90	69.5	11.4	1113 2 Q9CNR7	Q9CNR7 pasteurella
91	69.5	11.4	1179 2 Q13545	Q13545 homo sapien
92	69.5	11.4	1188 2 Q92656	Q92656 homo sapien
93	69.5	11.4	1188 2 Q92835	Q92835 homo sapien
94	69.5	11.4	1189 2 Q00145	Q00145 homo sapien
95	69.5	11.4	1189 2 Q9U0E0	Q9U0E0 homo sapien
96	69.5	11.4	1191 2 Q61181	Q61181 mus musculu
97	69.5	11.4	2647 2 Q9U4X0	Q9U4X0 plasmodium
98	69.5	11.4	2651 2 Q81EB6	Q81EB6 plasmodium
99	69.5	11.4	2770 2 Q7YUE9	Q7YUE9 plasmodium
100	69.5	11.4	2957 2 Q8WR56	Q8WR56 plasmodium

## ALIGNMENTS

```

RESULT 1
ID IL5_CANFA STANDARD; PRT; 134 AA.
AC 095J76;
DT 29-MAR-2004 (Rel. 43, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN Name-IL5;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21334408; PubMed=11440633; DOI=10.1089/107999001750277835;
RA Yang S., Sellins K.S., Weber E., McCall C.;
RT Canine interleukin-5: molecular characterization of the gene and
RT expression of biologically active recombinant protein.
RL J. Interferon Cytokine Res. 21:361-367(2001).
CC -1- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC -----
DR EMBL; AF331920; AAL10716.1; -.
DR EMBL; AF331919; AAL10715.1; -.
DR HSSP; P05113; 1HUL.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000166; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
DR Cytokine; Glycoprotein; Growth factor; Signal.
FT CHAIN 22 134 Interleukin-5.
FT SIGNAL 21 By similarity.
FT DISULFID 63 63 Interchain (with C-105) (By similarity).
FT DISULFID 105 105 Interchain (with C-63) (By similarity).
FT CARBOHYD 76 76 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 90 90 N-linked (GLCNAC...) (Potential).
SQ SEQUENCE 134 AA; 15307 MW; 003C86D94D6FAC6 CRC64;

Query Match 100.0%; Score 610; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.5e-53;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPMNRVATLTLLSTHRTWLTGGDNLMIPPTENKQHOLCIKVEFGIDTLKNQTA 60
DB 20 FAVENPMNRVATLTLLSTHRTWLTGGDNLMIPPTENKQHOLCIKVEFGIDTLKNQTA 79
QY 61 HGEAVDKLFQNLSTLKEHIEROKRCAGRWRYTKFLDYQLVFLGYINTEWTPES 115
DB 80 HGEAVDKLFQNLSTLKEHIEROKRCAGRWRYTKFLDYQLVFLGYINTEWTPES 134

RESULT 2
Q9TV10 PRELIMINARY; PRT; 118 AA.
AC 09TV10;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin-5 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF091133; AAD46991.1; -.
DR HSSP; P05113; 1HUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
FT NON_TER 1 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 13507 MW; 36A5563D67C968C CRC64;

Query Match 92.3%; Score 563; DB 2; Length 118;
Best Local Similarity 93.7%; Pred. No. 7.2e-49;
Matches 104; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAVENPMNRVATLTLLSTHRTWLTGGDNLMIPPTENKQHOLCIKVEFGIDTLKNQTA 60
DB 8 FAVENPMNRVATLTLLSTHRTWLTGGDNLMIPPTENKQHOLCIKVEFGIDTLKNQTA 67
QY 61 HGEAVDKLFQNLSTLKEHIEROKRCAGRWRYTKFLDYQLVFLGYINTEW 111
DB 68 HGEAVDKLFQNLSTLKEHIEROKRCAGRWRYTKFLDYQLVFLGYINTEW 118

RESULT 3
IL5_FELCA STANDARD; PRT; 134 AA.
AC 077515; 062740;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN Name-IL5;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98452719; PubMed=9781459;
RA Padrid P.A., Qin Y., Wells T.N.C., Solway J., Camoretti-Mercado B.;
RT Sequence and structural analysis of feline interleukin-5 cDNA.
RL Am. J. Vet. Res. 59:1263-1269(1998).
RN [2]
RP SEQUENCE OF 12-128 FROM N.A.
RA Harley R., Day M.J., Gruffydd-Jones T.J., Harbours D.A., Helps C.R.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC  
EMBL: AF025436; AAC64505.1; -  
DR HSSP; P05113; IHUL.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR000186; Interleukin\_5.  
DR Pfam; PF02025; IL5; 1.  
DR PRINTS; PR00432; INTERLEUKINS.  
DR Prodom; PD006721; Interleukin\_5; 1.  
KW Cytokine; Glycoprotein; Growth factor; Signal.  
FT SIGNAL 1 19 By similarity.  
FT CHAIN 20 134 Interleukin-5.  
FT DISULFID 63 63 Interchain (with C-105) (By similarity).  
FT DISULFID 105 105 Interchain (with C-63) (By similarity).  
FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).  
FT CONFLICT 104 105 KC -> NF (in Ref. 2).  
FT CONFLICT 108 111 ERWR -> KKKW (in Ref. 2).  
FT CONFLICT 114 114 K -> N (in Ref. 2).  
FT CONFLICT 117 117 D -> N (in Ref. 2).  
FT CONFLICT 121 121 V -> F (in Ref. 2).  
FT CONFLICT 125 126 VI -> LI (in Ref. 2).  
SQ SEQUENCE 134 AA; 15224 MW; 87D18DB8F8CAC820 CRC64;

Query Match 83.6%; Score 510; DB 1; Length 134;  
Best Local Similarity 84.1%; Pred. No. 1.8e-43;  
Matches 96; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 2 AVENPMRLVAETLLSTRHTWLIIGDNLMIPPEKNHQLCIKEVFGIDTLKNOTAH 61  
Db 21 AVGSPMRLVAETLLSTRHTWLIIGDNLMIPPEKNHQLCIKEVFGIDTLKNOTAH 80

Qy 62 GEAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYLVFGLVINTWTPES 115  
Db 81 GDAVEKLFQNLISLKEHIEROKRCAGERRVTKFLDYLVFGLVINTWTPES 134

## RESULT 4

Q9TSD7 PRELIMINARY; PRT; 134 AA.  
AC Q9TSD7;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Interleukin 5.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Vandevert E., Hughes K.J., O'Reilly K.L.;  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
EMBL: AF068770; AAC27616.1; -  
DR HSSP; P05113; IHUL.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR000186; Interleukin\_5.  
DR Pfam; PF02025; IL5; 1.  
DR PRINTS; PR00432; INTERLEUKINS.  
DR Prodom; PD006721; Interleukin\_5; 1.  
SQ SEQUENCE 134 AA; 15176 MW; 9A118B78F8CAC820 CRC64;

Query Match 82.8%; Score 505; DB 2; Length 134;  
Best Local Similarity 84.1%; Pred. No. 5.8e-43;  
Matches 95; Conservative 10; Mismatches 8; Indels 0; Gaps 0;  
Qy 2 AVENPMRLVAETLLSTRHTWLIIGDNLMIPPEKNHQLCIKEVFGIDTLKNOTAH 61  
Db 21 AVGSPMRLVAETLLSTRHTWLIIGDNLMIPPEKNHQLCIKEVFGIDTLKNOTAH 80

Db 21 AVGSPMRLVAETLLSTRHTWLIIGDNLMIPPEKNHQLCIKEVFGIDTLKNOTAH 80  
Qy 62 GEAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYLVFGLVINTWTPES 114  
Db 81 GDAVEKLFQNLISLKEHIEROKRCAGERRVTKFLDYLVFGLVINTWTPES 133

## RESULT 5

Q9MTM5 PRELIMINARY; PRT; 134 AA.  
AC Q9MTM5;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)  
DE Interleukin-5.  
GN Name-IL-5;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20130134; PubMed=10663563;  
RA Sylvain H., Matvienko O., Leonchiks A., Aylving K., van der Ploeg I.;  
RT "Molecular cloning, expression, and purification of pig interleukin-5";  
RT 5; "

Query Match 82.1%; Score 501; DB 2; Length 134;  
Best Local Similarity 85.1%; Pred. No. 1.5e-42;  
Matches 97; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 2 AVENPMRLVAETLLSTRHTWLIIGDNLMIPPEKNHQLCIKEVFGIDTLKNOTAH 61  
Db 21 AVGSPMRLVAETLLSTRHTWLIIGDNLMIPPEKNHQLCIKEVFGIDTLKNOTAH 80

Qy 62 GEAVDKLFQNLISLKEHIEROKRCAGERRVTKFLDYLVFGLVINTWTPES 115  
Db 81 GDAVEKLFQNLISLKEHIEROKRCAGERRVTKFLDYLVFGLVINTWTPES 134

## RESULT 6

IL5 HORSE STANDARD; PRT; 134 AA.  
AC 002699;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
DE (eosinophil differentiation factor).  
GN Name-IL5;  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
NCBI\_TaxID=9796;

Query Match 82.1%; Score 501; DB 2; Length 134;  
Best Local Similarity 85.1%; Pred. No. 1.5e-42;  
Matches 97; Conservative 7; Mismatches 10; Indels 0; Gaps 0;  
Qy 2 AVENPMRLVAETLLSTRHTWLIIGDNLMIPPEKNHQLCIKEVFGIDTLKNOTAH 61  
Db 21 AVGSPMRLVAETLLSTRHTWLIIGDNLMIPPEKNHQLCIKEVFGIDTLKNOTAH 80

```

RN [1]
RP SEQUENCE FROM N.A.
RA Vandergift E.V., Horohov D.W.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Factor that induces terminal differentiation of late-
CC      developing B-cells to immunoglobulin secreting cells (By
CC      similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC -----
CC EMBL; U91947; AAB51382.1; -.
CC HSP; P05133; 1HU.
CC InterPro: IPR009079; 4 helix cytokine.
CC InterPro: IPR000186; Interleukin_5.
CC Pfam: PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKINS.
CC ProDom; PD006721; Interleukin_5; 1.
CC Cytokine; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 19 By similarity.
CC CHAIN 20 134 Interchain (with C-105) (By similarity).
CC DISULFID 63 63 Interchain (with C-63) (By similarity).
CC DISULFID 105 105 Interchain (with C-63) (By similarity).
CC CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
CC SEQUENCE 134 AA; 15081 MW; 2914840E3E7A006D CRC64;

Query Match 81.0%; Score 494; DB 1; Length 134;
Best Local Similarity 84.1%; Pred. No. 7.5e-42;
Matches 95; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 AVENPNRRLVATLTLLSTHRTWLIGDGNLMTPTPKNKHQLCIKKVFQIDTLKQNTAH 61
DB 21 AVESPMNRRLVATLTLLSTHRTWLIGDGNLMTPTPKNKHQLCIKKVFQIDTLKQNTAH 80
QY 62 GRAVDKLFONTSLIKHEIRKRCAGGRWVTKFDYLVQVFLGVINTWTPES 114
DB 81 GBAVAKLFONTSLIKHEIRKRCAGGRWVTKFDYLVQVFLGVINTWTPES 133

RESULT 7
IL5_BOVIN STANDARD; PRT; 134 AA.
AC P52173;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Bosinophil differentiation factor).
GN Name=IL5;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
OX [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Blood;
RA MEDLINE=97075944; PubMed=8918267; DOI=10.1016/0378-1119(96)00252-1;
RA Mertens B., Gohrlicht B., Seow H.F.;
RT "The nucleotide sequence of the bovine interleukin-5-encoding cDNA.";
RL Gene 176:273-274(1996).
CC -1- FUNCTION: Factor that induces terminal differentiation of late-
CC      developing B-cells to immunoglobulin secreting cells (By
CC      similarity).

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CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC -----
CC EMBL; Z67872; CAA91779.1; -.
CC PIR; JCS116; JCS116.
CC HSP; P05116; 1HU.
CC InterPro: IPR009079; 4 helix cytokine.
CC InterPro: IPR000186; Interleukin_5.
CC Pfam: PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKINS.
CC ProDom; PD006721; Interleukin_5; 1.
CC Cytokine; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 21 By similarity.
CC CHAIN 22 134 Interchain (with C-105) (By similarity).
CC DISULFID 63 63 Interchain (with C-63) (By similarity).
CC DISULFID 105 105 Interchain (with C-63) (By similarity).
CC CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
CC SEQUENCE 134 AA; 15229 MW; 0B3A2328E7431F4 CRC64;

Query Match 80.5%; Score 491; DB 1; Length 134;
Best Local Similarity 81.6%; Pred. No. 1.5e-41;
Matches 93; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 2 AVENPNRRLVATLTLLSTHRTWLIGDGNLMTPTPKNKHQLCIKKVFQIDTLKQNTAH 61
DB 21 AVESPMNRRLVATLTLLSTHRTWLIGDGNLMTPTPKNKHQLCIKKVFQIDTLKQNTAH 80
QY 62 GRAVDKLFONTSLIKHEIRKRCAGGRWVTKFDYLVQVFLGVINTWTPES 115
DB 81 GBAVAKLFONTSLIKHEIRKRCAGGRWVTKFDYLVQVFLGVINTWTPES 134

RESULT 8
IL5_SHEEP STANDARD; PRT; 132 AA.
AC Q28586;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Bosinophil differentiation factor).
GN Name=IL5;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OC NCBI_TaxID=9940;
OX [1]
RP SEQUENCE FROM N.A.
RA Bryson C.E., Viney E., Brandon M., Boyd A.W.;
RA Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Seow H.-F., David M.-J., McWaters P.G., Hurst L., Wood P.R.;
RT "Cloning of ovine interleukin-5 cDNA.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Factor that induces terminal differentiation of late-
CC      developing B-cells to immunoglobulin secreting cells (By
CC      similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-5 family.

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DR EMBL: U17053; AAB60629.1; -.  
DR EMBL: U17052; AAB60629.1; JOINED.  
DR EMBL: U35038; AAC99991.1; -.  
DR HSSP; P05113; 1HUL.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR00186; Interleukin\_5.  
DR Pfam; PF02025; IL5; 1.  
DR PRINTS; PRO0432; INTERLEUKINS.  
DR ProDom; PD006721; Interleukin\_5; 1.  
KW Cytokine; Glycoprotein; Growth factor; Signal.  
FT SIGNAL 1 19 By similarity.  
FT CHAIN 20 132 Interleukin-5.  
FT DISULFID 61 61 Interchain (with C-103) (By similarity).  
FT DISULFID 103 103 Interchain (with C-61) (By similarity).  
FT CARBOHYD 74 74 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 132 AA; 14974 MW; D783F2B720E249D9 CRC64;

Query Match 79.8%; Score 487; DB 1; Length 132;  
Best Local Similarity 80.7%; Pred. No. 3.7e-41;  
Matches 92; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 2 AVENPRLVAETLTLLSTHRTWLTIGDGNLMIPTPENKNOHCIRKVEFGIDTLKNOTAH 61  
Db 19 AVSTNRLVAETLTLLSTHRTWLTIGDGNLMIPTPENKNOHCIRKVEFGIDTLKNOTAQ 78  
Qy 62 GEAVDKLFOISLTIKHIKEROXKCGRRMRYKFLDYLOVFLGVINTWTPES 115  
Db 79 GDAVKKIFRNLSTIKHYIDLRKRCGGRMRVKQFLDYLOVFLGVINTWTPES 132

## RESULT 9

Q8MKH1 PRELIMINARY; PRT; 134 AA.  
AC Q8MKH1;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Interleukin-5.  
OS Saimiri sciureus (Common squirrel monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.  
NCBI\_TaxID=9521;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-Y;  
RA Hezaud J.M., Laveigne A., Kazanji M.;  
RT "Molecular cloning, characterization, and quantification of squirrel  
RT monkey (Saimiri sciureus) Th1 and Th2 cytokines."  
RL Immunogenetics 54:20-29(2002).  
DR EMBL; AF294756; AAK92043.1; -.  
DR HSSP; P05113; 1HUL.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005137; P:interleukin-5 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR00186; Interleukin\_5.  
DR Pfam; PF02025; IL5; 1.  
DR PRINTS; PRO0432; INTERLEUKINS.  
DR ProDom; PD006721; Interleukin\_5; 1.  
SQ SEQUENCE 134 AA; 15210 MW; EAPACASDB48767C CRC64;

Query Match 62.6%; Score 382; DB 2; Length 134;  
Best Local Similarity 68.2%; Pred. No. 1.5e-30;  
Matches 75; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

Qy 6 PMRLVAETLTLLSTHRTWLTIGDGNLMIPTPENKNOHCIRKVEFGIDTLKNOTAHGAV 65  
Db 25 PSLVAETLTLLSTHRTWLTIGDGNLMIPTPENKNOHCIRKVEFGIDTLKNOTAQSSGV 84  
Qy 66 DKLFONSLTIKHIKEROXKCGRRMRYKFLDYLOVFLGVINTWTPES 115  
Db 85 EKLFONSLTIKHIKEROXKCGRRMRYKFLDYLOVFLGVINTWTPES 134

## RESULT 10

IL5\_CAVPO STANDARD; PRT; 135 AA.  
AC 008587;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
DE (Eosinophil differentiation factor).  
GN Name=IL5;  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96289181; PubMed=8764226;  
RA Mansour M., Karmilowicz M., Hawrylik S.J., Nalcercio B., Angilly J.,  
RA Conklyn M.J., Lilly C.M., Drazen J.M., Lee S.B., Auperin D.D.,  
RA de Wet J.R., Cohen V.D., Showell H.J., Danley D.B.;  
RT "Production and characterization of guinea pig IL-5 in baculovirus-  
RT infected insect cells."  
RL Am. J. Physiol. 270:L1002-L1007(1996).  
CC -1- FUNCTION: Factor that induces terminal differentiation of late-  
CC developing B-cells to immunoglobulin secreting cells (By  
CC similarity).  
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the IL-5 family.

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CC or send an email to [license@1sb-sib.ch](mailto:license@1sb-sib.ch)).

DR EMBL; U34588; AAB61357.1; -.  
DR HSSP; P05113; 1HUL.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR00186; Interleukin\_5.  
DR Pfam; PF02025; IL5; 1.  
DR PRINTS; PRO0432; INTERLEUKINS.  
DR ProDom; PD006721; Interleukin\_5; 1.  
KW Cytokine; Glycoprotein; Growth factor; Signal.  
FT SIGNAL 1 19 By similarity.  
FT CHAIN 20 135 Interleukin-5.  
FT DISULFID 64 64 Interchain (with C-106) (By similarity).  
FT DISULFID 106 106 Interchain (with C-64) (By similarity).  
FT CARBOHYD 48 48 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 77 77 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 91 91 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 135 AA; 15291 MW; EB8525213252731 CRC64;

Query Match 61.0%; Score 372; DB 1; Length 135;  
Best Local Similarity 68.5%; Pred. No. 1.5e-29;  
Matches 74; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

Qy 7 MRLVAETLTLLSTHRTWLTIGDGNLMIPTPENKNOHCIRKVEFGIDTLKNOTAHGAV 66  
Db 27 LRLVAETLTLLSTHRTWLTIGDGNLMIPTPENKNOHCIRKVEFGIDTLKNOTAQSSGV 86

QY 67 KLFONSLIKSHIEROKKRCAGERRWTKFDLYQVFLGYINTWTPB 114  
DB 87 TLFONSLIKKHIDLOKOKGERRRRVQPLDYLOEFLAVINTWTEB 134

## RESULT 11

IL5\_CERTO STANDARD; PRT; 134 AA.

AC 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
DE (Bosniophil differentiation factor).  
GN Name=IL5;  
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
OC Bakayotea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Cercopithecus.  
OX NCBI\_TaxID=9531;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FUJ;  
RX MEDLINE=96003435; PubMed=7561102;  
RA Villinger F.J., Bier S.S., Wayne A.B., Chikkala N., Ansari A.A.;  
RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates."  
RT J. Immunol. 155:3946-3954 (1995).  
RL -1- FUNCTION: Factor that induces terminal differentiation of late-developing B-cells to immunoglobulin secreting cells (By similarity).  
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the IL-5 family.

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CC -----  
CC EMBL: L26033; AAA99971.1; -.  
DR HSSP; P05113; 1HU.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR000186; Interleukin\_5.  
DR Pfam; PF02025; IL5; 1.  
DR PRINTS; PRO0432; INTERLEUKINS.  
DR ProDom; PD06721; Interleukin\_5; 1.  
KW Cytokine; Glycoprotein; Growth factor; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 134 Interleukin-5.  
FT DISULFID 63 63 Interchain (with C-105) (By similarity).  
FT DISULFID 103 103 Interchain (with C-63) (By similarity).  
FT CARBOHYD 22 22 O-linked (By similarity).  
FT CARBOHYD 47 47 O-linked (GlcNAc...) (Potential).  
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 134 AA; 15339 MW; 7BD0491C437981ED CRC64;

Query Match 59.2%; Score 361; DB 1; Length 134;  
Best Local Similarity 63.4%; Pred. No. 1.9e-28;  
Matches 71; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 4 ENPMNRLVAETLLSTHRTWTLGDGNLMTPTENKNHOCIGKEVFGIDTLKNQTAH 63  
DB 23 EITPSALVKEITLTLSTHRTLLTGNETLRIPVPHKHQCTSEITFGIGTLSSQTLQGS 82  
QY 64 AVDKLFONSLIKSHIEROKKRCAGERRWTKFDLYQVFLGYINTWTPB 115  
DB 83 TVRFLFONSLIKKHIDLOKOKGERRRRVQPLDYLOEFLAVINTWTEB 134

RESULT 12  
IL5\_MERUN STANDARD; PRT; 132 AA.

AC 062575;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
DE (Bosniophil differentiation factor).  
GN Name=IL5;  
OS Meriones unguliculatus (Mongolian jird) (Mongolian gerbil).  
OC Bakayotea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;  
OC Meriones.  
OX NCBI\_TaxID=10047;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Mai Z., Klei T.R.;  
RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Factor that induces terminal differentiation of late-developing B-cells to immunoglobulin secreting cells (By similarity).  
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the IL-5 family.

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CC -----  
CC EMBL: I37780; AAA65675.1; -.  
DR HSSP; P05113; 1HU.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR000186; Interleukin\_5.  
DR Pfam; PF02025; IL5; 1.  
DR PRINTS; PRO0432; INTERLEUKINS.  
DR ProDom; PD06721; Interleukin\_5; 1.  
KW Cytokine; Glycoprotein; Growth factor; Signal.  
FT SIGNAL 1 17 Potential.  
FT CHAIN 18 132 Interleukin-5.  
FT DISULFID 61 61 Interchain (with C-103) (By similarity).  
FT DISULFID 103 103 Interchain (with C-61) (By similarity).  
FT CARBOHYD 45 45 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 74 74 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 132 AA; 15164 MW; 60CE3852F9F84261 CRC64;

Query Match 58.7%; Score 358; DB 1; Length 132;  
Best Local Similarity 61.1%; Pred. No. 3.8e-28;  
Matches 69; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 2 AVENPMNRLVAETLLSTHRTWTLGDGNLMTPTENKNHOCIGKEVFGIDTLKNQTAH 61  
DB 19 ALEIPMSAVVKEITLQSLSTHRTLLTSEVTRLRIPVPHKHQCTSEITFGIGTLIDLNQTAH 78  
QY 62 GEAVDKLFONSLIKSHIEROKKRCAGERRWTKFDLYQVFLGYINTWTPB 114  
DB 79 GGAVERTLFONSLIKKHIDLOKOKGERRRRARQPLDYLOEFLAVINTWTEB 131

RESULT 13  
IL5\_HUMAN STANDARD; PRT; 134 AA.

AC P05113; Q13840;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)

DE (Eosinophil differentiation factor) (B cell differentiation factor 1).  
 GN Name=IL5;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87066782; PubMed=3024129;  
 RA Azuma C., Tanabe T., Konishi M., Kinashi T., Noma T., Matsuda F.,  
 RA Yachi Y., Takatsu K., Hammarstrom L., Smith C.I.E., Severinson E.,  
 RA Honjo T.;  
 RT "Cloning of cDNA for human T-cell replacing factor (interleukin-5) and  
 RT comparison with the murine homologue."  
 RL Nucleic Acids Res. 14:9149-9158(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88059042; PubMed=2824500;  
 RA Tanabe T., Konishi M., Mizuta T., Noma T., Honjo T.;  
 RT "Molecular cloning and structure of the human interleukin-5 gene."  
 RL J. Biol. Chem. 262:16580-16584(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88016145; PubMed=3496940;  
 RA Campbell H.D., Tucker W.Q.J., Hort Y., Martinson M.E., Mayo G.,  
 RA Cluttenbuck E.J., Sanderson C.J., Young I.G.;  
 RT "Molecular cloning, nucleotide sequence, and expression of the gene  
 RT encoding human eosinophil differentiation factor (interleukin 5)."  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6629-6633(1987).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88041112; PubMed=2823259;  
 RA Yokota K., Coffman R.L., Hagiwara H., Rennick D.M., Takebe Y.,  
 RA Hoy P., Pene J., Briere F., Shradar B., Yang G., Meyerson P., Lin J.,  
 RA Lee F.D., Arai N., Arai K.;  
 RT "Isolation and characterization of lymphokine cDNA clones encoding  
 RT mouse and human IgA-enhancing factor and eosinophil colony-stimulating  
 RT factor activities: relationship to interleukin 5."  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7388-7392(1987).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Honjo T., Takatsu K., Severinson E.;  
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
 RA Nickerson D.A.;  
 RT "SeaclegSPs, NHLBI HL66682 program for genomic applications, UM-  
 RT FHCRG, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE OF 20-134, AND DISULFIDE BONDS.  
 RX MEDLINE=90299868; PubMed=2361960;  
 RA Minamitake Y., Kodama S., Katayama T., Adachi H., Tanaka S.,  
 RA Teujimoto M.;  
 RT "Structure of recombinant human interleukin 5 produced by Chinese  
 RT hamster ovary cells."  
 RL J. Biochem. 107:292-297(1990).  
 RN [8]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=9123878; PubMed=2037074; DOI=10.1016/0014-5793(91)80553-F;  
 RA Proudfoot A.E.I., Davies J.G., Turcatti G., Wingfield P.T.;  
 RT "Human interleukin-5 expressed in *Escherichia coli*: assignment of the  
 RT disulfide bridges of the purified unglycosylated protein."  
 RL FEBS Lett. 283:61-64(1991).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
 RX MEDLINE=93247642; PubMed=8483502; DOI=10.1038/363172a0;  
 RA Milburn M.V., Hasseil A.M., Lambert M.H., Jordan S.R.,  
 RA Proudfoot A.E.I., Graber P., Wells T.N.C.;  
 RT "A novel dimer configuration revealed by the crystal structure at 2.4-  
 RT A resolution of human interleukin-5.";

RL Nature 363:172-176(1993).  
 CC -1- FUNCTION: Factor that induces terminal differentiation of late-  
 CC developing B-cells to immunoglobulin secreting cells.  
 CC -1- SUBUNIT: Homodimer; disulfide-linked.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the IL-5 family.  
 CC -1- DATABASE: NARS=Rad Systems' cytokine mini-reviews: IL5;  
 CC WWW=[http://www.rndsystems.com/asp/g\\_situbody.asp?bodyid=207](http://www.rndsystems.com/asp/g_situbody.asp?bodyid=207).  
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DR EMBL: X04688; CAA28390.1; -;  
 DR EMBL: J03478; AAA74469.1; -;  
 DR EMBL: J02971; AAA98620.1; -;  
 DR EMBL: X12705; CAA31210.1; -;  
 DR EMBL: X12705; CAA31211.1; -;  
 DR EMBL: AF53265; AAK19759.1; -;  
 DR PIR: A28477; A28477.  
 DR PIR: 1H0L; X-ray; A/B=24-131.  
 DR Genew; HGNC:6016; IL5.  
 DR MIM: 147850; -;  
 DR GO: GO:0005576; C:extracellular; TAS.  
 DR GO: GO:0005137; F:interleukin-5 receptor binding; TAS.  
 DR GO: GO:0006262; P:hyperresponsive response; TAS.  
 DR GO: GO:0006954; P:inflammatory response; TAS.  
 DR InterPro: IPR009079; 4 helix cytokine.  
 DR InterPro: IPR00186; Interleukin\_5.  
 DR Pfam: PF02025; IL5; 1.  
 DR PRINTS: PR00432; INTERLEUKINS.  
 DR ProDom: PD006721; Interleukin\_5; 1.  
 DR 3D-structure; Cytokine; Direct protein sequencing; Glycoprotein;  
 KM Growth factor; Signal.  
 FT STGMAL 1 19  
 FT CHAIN 20 134 Interleukin-5.  
 FT DISULFID 63 63 Interchain (with C-105).  
 FT CARBOHYD 105 105 Interchain (with C-63).  
 FT CARBOHYD 22 22 O-linked.  
 FT CARBOHYD 47 47 N-linked (GlcNAc...).  
 FT CONFLICT 88 88 F -> L (in Ref. 5; CAA31210).  
 FT HELIX 26 38  
 FT TURN 39 40  
 FT HELIX 41 45  
 FT TURN 46 46  
 FT STRAND 51 54  
 FT HELIX 60 62  
 FT HELIX 64 77  
 FT TURN 82 82  
 FT HELIX 83 103  
 FT TURN 104 105  
 FT STRAND 108 111  
 FT HELIX 112 128  
 FT TURN 129 129  
 SQ SEQUENCE 134 AA; 15238 MW; DC984467179556A3 CRC64;

Query Match 58.4%; Score 356; DB 1; Length 134;  
 Best local Similarity 62.5%; Pred. No. 6, 1e-28;  
 Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY	4	ENDPNRLVAVETLLSTHRTWTLIGDGNLMIPPEPNKHOLCTKEVFGIDTLKNQTAHGR	63
DB	23	EIPTSALVETETALLSTHRTLLANETLRIPVAVHKNHOLCTEIRIIGIGTLESSQTVQCG	82
QY	64	AVDKLQNLSTLKEHIEROKKQAGRWVTKLDYLOFLGVINTEWTPES	115
DB	83	TYERLPKNLSLTKKYIDGKKKCGERRRVNDFLYLOSLFVGNTEWTEES	134

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RESULT 14
ID IL5_SIGH1 STANDARD; PRT; 132 AA.
AC Q9E619;
DT 28-FEB-2003 (Rel. 41, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN Name:IL5;
OS Sigmodon hispidus (Haploid cotton rat).
OC Burkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RA PubMed=11054577; DOI=10.1016/S0378-1119(00)00366-8;
RA Howard S., Jacques A., Haumont M., Daminet V., Millican F., Glineur F.,
RA Bollen A.;
RT Cloning, expression and purification of recombinant cotton rat
RT Interleukin-5;
RT Gene 257:149-155(2000).
CC -1- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF148211; AAG16722.1; -.
DR HSSP; P05113; 1HUL.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 132 Interleukin-5.
FT DISULFID 61 61 Interchain (with C-103) (By similarity).
FT DISULFID 103 103 Interchain (with C-61) (By similarity).
FT CARBOHYD 45 45 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 74 74 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 132 AA; 15434 MW; B328B81B371FFB9 CRC64;

Query Match 58.0%; Score 354; DB 1; Length 132;
Best Local Similarity 59.6%; Pred. No. 9.6e-28;
Matches 68; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

QY 1 PAVENMNLVAETTLTSTHRTWILGGDGLMTPTPENKHOCTIEVEGIDTLKNOQA 60
DB 18 FAVEIEMHVVVETLLQLSTHRTLLTSNETVRLPVTHKNHQLCIGEIFRGDLINKQTV 77

QY 61 HGEAVDKLFONTSLIKHEIEROKKRCAGERRVTKFADYLVQVLYINTEWTPR 114
DB 78 RGCTVETLRFNLSLIKTIYIDROKCKGERRRRTRQFLDYLGRTVWGTEWTPR 131

RESULT 15
ID IL5_MACMU STANDARD; PRT; 134 AA.
AC P48093;
DT 01-FEB-1996 (Rel. 33, Created)

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DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN Name:IL5;
OS Macaca mulatta (rhesus macaque).
OC Burkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RT J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SIMILARITY: Belongs to the IL-5 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U19848; AAA86710.1; -.
DR HSSP; P05113; 1HUL.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 134 Interleukin-5.
FT DISULFID 63 63 Interchain (with C-105) (By similarity).
FT DISULFID 105 105 Interchain (with C-63) (By similarity).
FT CARBOHYD 47 47 O-linked (By similarity).
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 134 AA; 15150 MW; DC985ECF4AB86A3 CRC64;

Query Match 57.7%; Score 352; DB 1; Length 134;
Best Local Similarity 62.5%; Pred. No. 1.5e-27;
Matches 70; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 4 ENPMNRVAVETTLTSTHRTWILGGDGLMTPTPENKHOCTIEVEGIDTLKNOQA 63
DB 23 EIPASLVVETLLTSTHRTLLIANETLPIPVVHKNHQLCTIEVFGIGLESQTVQGG 82

QY 64 AVDKLFONTSLIKHEIEROKKRCAGERRVTKFADYLVQVLYINTEWTPR 115
DB 83 TVERLRFNLSLIKTIYIDROKCKGERRRRVNOFLDYLGRTVWGTEWTPR 134

Search completed: August 4, 2005, 17:11:06
Job time : 105.378 secs

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12	610	87.6	345	4	US-09-451-527-85	Sequence 85, App
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QY 1 MetArgMetLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20

Sequence 87, Appl. Sequence 1235, Appl. Sequence 4, Appl. Sequence 21, Appl. Sequence 39, Appl. Sequence 31, Appl. Sequence 41, Appl. Sequence 43, Appl. Sequence 45, Appl. Sequence 49, Appl. Sequence 57, Appl. Sequence 53, Appl. Sequence 29, Appl. Sequence 51, Appl. Sequence 47, Appl. Sequence 5, Appl. Sequence 8, Appl. Patent No. 5324644, Patent No. 5324644, Patent No. 5324644, Sequence 475, Appl. Sequence 61, Appl. Sequence 15318, Appl.

Db 1 ATGGAATGCTTCGAATTGAGTTTGCTAGCTCTGGGCGCTAGTGTTCGCTTT 60  
Qy 21 AAlaValGluAenPromeAaArgLeuValAlaGluThrLeuThrLeuSerThHis 40  
Db 61 GCTTGAATAATCCCATGAAATAGACTGGTGGCAAGACCTTGACACTGCTCTCACTCAT 120  
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60  
Db 121 CGAACTGGCTGATAGGCGATGGGAACCTGATGATTCTTCACTCTGAAAAATAAAAATCAC 180  
Qy 61 GlnLeuCySilelysgluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80  
Db 181 CAACGTGCATTAAGAAAGATTTCAGGGTATTAACACATTGAAGAAACCAACGCGCCAC 240  
Qy 81 GlyGluAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100  
Db 241 GGGAGGCTGTGGATTAACCTATTCCTCAAACTTGCTTTAATAAAGAACACATAGAGCGC 300  
Qy 101 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120  
Db 301 CAAAAAAGAGGTGTGCGAGGAAGATGAGAGTGAACAAAGTTCTTAGACTTACCTGCA 360  
Qy 121 ValPheLeuGlyValIleAsnThrGluTyrThrProGluSer 134  
Db 361 GTATTCTTGTTGTAATTAACACCGAGTGAACCGGAAGT 402

## RESULT 2

US-09-322-409-84/C  
Sequence 84, Application US/09322409  
Patent No. 6471957

GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee

APPLICANT: Yang, Shumin

APPLICANT: Drelitz, Matthew J.

APPLICANT: Wonderling, Ramani S.

TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

FILE REFERENCE: IM-2-C1

CURRENT APPLICATION NUMBER: US/09/322,409

EARLIER FILING DATE: 1999-05-28

EARLIER APPLICATION NUMBER: 60/087,306

NUMBER OF SEQ ID NOS: 154

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 84

LENGTH: 402

TYPE: DNA

ORGANISM: Canis familiaris

US-09-322-409-84

## Alignment Scores:

Pred. No.: 3,15e-93 Length: 402  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-787-382-5 (1-134) x US-09-322-409-84 (1-402)

Qy 1 MeArgMetLeuAenLeuSerLeuLeuAlaGluAlaIleTyrValSerAlaPhe 20  
Db 402 ATGGAATGCTTCGAATTGAGTTTGCTAGCTCTGGGCGCTAGTGTTCGCTTT 343  
Qy 21 AAlaValGluAenPromeAaArgLeuValAlaGluThrLeuThrLeuSerThHis 40  
Db 342 GCTTGAATAATCCCATGAAATAGACTGGTGGCAAGACCTTGACACTGCTCTCACTCAT 283  
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60  
Db 282 CGAACTGGCTGATAGGCGATGGGAACCTGATGATTCTTCACTCTGAAAAATAAAAATCAC 223  
Qy 61 GlnLeuCySilelysgluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80

Db 222 CAACGTGCATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAACCTGCCAC 163  
Qy 81 GlyGluAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100  
Db 162 GGGAGGCTGTGATTAACCTATTCCTCAAACTTGCTTTAATAAAGAACACATAGAGCGC 103  
Qy 101 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120  
Db 102 CAAAAAAGAGGTGTGCGAGGAAGATGAGAGTGAACAAAGTTCTTAGACTTACCTGCA 43  
Qy 121 ValPheLeuGlyValIleAsnThrGluTyrThrProGluSer 134  
Db 42 GTATTCTTGTTGTAATTAACACCGAGTGAACCGGAAGT 1

## RESULT 3

US-09-451-527-83  
Sequence 83, Application US/09451527  
Patent No. 6482403

GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee

APPLICANT: Yang, Shumin

APPLICANT: Drelitz, Matthew J.

APPLICANT: Wonderling, Ramani S.

TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

FILE REFERENCE: IM-2-C2

CURRENT APPLICATION NUMBER: US/09/451,527

EARLIER FILING DATE: 1999-12-01

EARLIER APPLICATION NUMBER: 09/322,409

EARLIER FILING DATE: 1999-05-28

EARLIER APPLICATION NUMBER: 60/087,306

NUMBER OF SEQ ID NOS: 174

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 83

LENGTH: 402

TYPE: DNA

ORGANISM: Canis familiaris

US-09-451-527-83

## Alignment Scores:

Pred. No.: 3,15e-93 Length: 402  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-787-382-5 (1-134) x US-09-451-527-83 (1-402)

Qy 1 MeArgMetLeuAenLeuSerLeuLeuAlaGluAlaIleTyrValSerAlaPhe 20  
Db 1 ATGGAATGCTTCGAATTGAGTTTGCTAGCTCTGGGCGCTAGTGTTCGCTTT 60  
Qy 21 AAlaValGluAenPromeAaArgLeuValAlaGluThrLeuThrLeuSerThHis 40  
Db 61 GCTTGAATAATCCCATGAAATAGACTGGTGGCAAGACCTTGACACTGCTCTCACTCAT 120  
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60  
Db 121 CGAACTGGCTGATAGGCGATGGGAACCTGATGATTCTTCACTCTGAAAAATAAAAATCAC 180  
Qy 61 GlnLeuCySilelysgluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80  
Db 181 CAACGTGCATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAACGCGCCAC 240  
Qy 81 GlyGluAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100  
Db 241 GGGAGGCTGTGATTAACCTATTCCTCAAACTTGCTTTAATAAAGAACACATAGAGCGC 300  
Qy 101 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120

Db 301 CAAAAAAGGTGTCAGAGAAAGATGAGATGACCAAGTCTTACCTGCA 360  
Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
Db 361 GTATTTCTTGCTGATTAACACCGAGTGCACCGGAAAGT 402

RESULT 4  
US-09-451-527-84/C  
; Sequence 84, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Gek-Kea  
; APPLICANT: Yang, Shumin  
; APPLICANT: Drelitz, Matthew J.  
; APPLICANT: Ramani, S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-451-527-84

Alignment Scores:  
Pred. No.: 3,15e-93 Length: 402  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 4

US-10-787-382-5 (1-134) x US-09-451-527-84 (1-402)

Qy 1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyValIleAsnThrValSerAlaPhe 20  
Db 402 ATGGAGATGCTTGAATTTAGATTGCTACCTCTTGCGGCTGCTGATGTTTCTGCTT 343  
Qy 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
Db 342 GCTGTAGAAATCCCATGATAGACTGGTGCAAGACTTGACACTGCTCTCCACTCAT 283  
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60  
Db 282 CGAAGTGGCTGATGAGGCGATGGGAACTGATGATCTTCTACTCTCGAAATTAATTAATC 223  
Qy 61 GlnLeuCysIleLeuGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80  
Db 222 CAACGTGCATTTAAAGAACTTTTTCAGGGATATAGACATTTGAAGAACCAACCTGCCAC 163  
Qy 81 GlyIuAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100  
Db 162 GGGGAGGCTGTGATTAACCTATTCCTTAAATTAAGAACACATGAGCGC 103  
Qy 101 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120  
Db 102 CAAAAAAGGTGTCAGAGAAAGATGAGATGAGAACCAAGTTCTTACTACTGCA 43  
Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
Db 42 GTATTTCTTGCTGATTAACACCGAGTGCACCGGAAAGT 1

RESULT 5  
US-09-322-409-80  
; Sequence 80, Application US/09322409

Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Gek-Kea  
; APPLICANT: Yang, Shumin  
; APPLICANT: Drelitz, Matthew J.  
; APPLICANT: Ramani, S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; NAME/KEY: CDS  
; LOCATION: (29) .. (430)  
US-09-322-409-80

Alignment Scores:  
Pred. No.: 6,03e-93 Length: 610  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 4

US-10-787-382-5 (1-134) x US-09-322-409-80 (1-610)

Qy 1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyValIleAsnThrValSerAlaPhe 20  
Db 29 ATGGAGATGCTTGAATTTAGATTGCTACCTCTTGCGGCTGCTGATGTTTCTGCTT 88  
Qy 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
Db 89 GCTGTAGAAATCCCATGATAGACTGGTGCAAGACTTGACACTGCTCTCCACTCAT 148  
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60  
Db 149 CGAAGTGGCTGATGAGGCGATGGGAACTGATGATCTTCTACTCTCGAAATTAATTAATC 208  
Qy 61 GlnLeuCysIleLeuGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80  
Db 209 CAACGTGCATTTAAAGAACTTTTTCAGGGATATAGACATTTGAAGAACCAACCTGCCAC 268  
Qy 81 GlyIuAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100  
Db 269 GGGGAGGCTGTGATTAACCTATTCCTTAAATTAAGAACACATGAGCGC 328  
Qy 101 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120  
Db 329 CAAAAAAGGTGTCAGAGAAAGATGAGATGAGAACCAAGTTCTTACTACTGCA 388  
Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
Db 389 GTATTTCTTGCTGATTAACACCGAGTGCACCGGAAAGT 430

RESULT 6  
US-09-322-409-82/C  
; Sequence 82, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Gek-Kea  
; APPLICANT: Yang, Shumin  
; APPLICANT: Drelitz, Matthew J.  
; APPLICANT: Ramani, S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF

```
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/09/322,409
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 82
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
US-09-322-409-82

Alignment Scores:
Pred. No.: 6,03e-93 Length: 610
Score: 696.00 Matches: 134
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-787-382-5 (1-134) x US-09-322-409-82 (1-610)

QY 1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaIleTyrValSerAlaPhe 20
DB 582 ATGAGAAATGCTTCTGAAATTTGAGTTTGCTACCTCTGGGCGCTATGTTTCTGCCCTT 523
QY 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
DB 522 GCTGTAGAAAATCCCATGAATAGACTGTGTGAGAGACCTTGACACTGCTCCATGTTTCAAT 463
QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleYsaHis 60
DB 462 CGAAGCTTGGCTGATAGGCGATGGAGACCTGATGATTCCTACTCTGAAAATAAAAATCAC 403
QY 61 GlnLeuCySilelyGluValPheGlnGlyIleAspThrLeuIleYsaGlnThrAlaHis 80
DB 402 CAACGTGCATTAAGAAAGTTTTCAGGGTATGACACATTTGAAGAACCAAACTGCCAC 343
QY 81 G1G1u1a1aVala1aP1y1e1uPheG1nAsnLeuSerLeuIleYsG1uH1s11eG1uArg 100
DB 342 GGGAGGCTGTGATTAACCTATTCCTCAAACTTCTTTAATTAAGAACACATAGAGCC 283
QY 101 GlnlylsyarsGysalaglyGluArgTrpArgValThrlyspheLeuAspTyrLeuGln 120
DB 282 CAAAAAAAAGGTGTGAGAGAGAAAGATGAGAGTGAACAAAGTCTTAGACTTACCTGCAA 223
QY 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
DB 222 GTATTCTTGTGTATTAACACGAGTGAACACCGGAAAGT 181

RESULT 7
US-09-451-527-80
Sequence 80, Application US/09451527
Patent No. 6482403
GENERAL INFORMATION:
APPLICANT: Yang, Gek-Kee
APPLICANT: Sim, Gek-Shumlin
APPLICANT: Drelitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/09/451,527
EARLIER FILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 09/322,409
EARLIER FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 80
LENGTH: 610
```

```
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (29)..(430)
US-09-451-527-80

Alignment Scores:
Pred. No.: 6,03e-93 Length: 610
Score: 696.00 Matches: 134
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-787-382-5 (1-134) x US-09-451-527-80 (1-610)

QY 1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaIleTyrValSerAlaPhe 20
DB 29 ATGAGAAATGCTTCTGAAATTTGAGTTTGCTACCTCTGGGCGCTATGTTTCTGCCCTT 88
QY 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
DB 89 GCTGTAGAAAATCCCATGAATAGACTGTGTGAGAGACCTTGACACTGCTCCATGCTCAT 148
QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleYsaHis 60
DB 149 CGAAGCTTGGCTGATAGGCGATGGAGACCTGATGATTCCTACTCTGAAAATAAAAATCAC 208
QY 61 GlnLeuCySilelyGluValPheGlnGlyIleAspThrLeuIleYsaGlnThrAlaHis 80
DB 209 CAACGTGCATTAAGAAAGTTTTCAGGGTATGACACATTTGAAGAACCAAACTGCCAC 268
QY 81 G1G1u1a1aVala1aP1y1e1uPheG1nAsnLeuSerLeuIleYsG1uH1s11eG1uArg 100
DB 269 GGGAGGCTGTGATTAACCTATTCCTCAAACTTCTTTAATTAAGAACACATAGAGCC 328
QY 101 GlnlylsyarsGysalaglyGluArgTrpArgValThrlyspheLeuAspTyrLeuGln 120
DB 329 CAAAAAAAAGGTGTGAGAGAGAAAGATGAGAGTGAACAAAGTCTTAGACTTACCTGCAA 388
QY 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
DB 389 GTATTCTTGTGTATTAACACCGAGTGAACACCGGAAAGT 430

RESULT 8
US-09-451-527-82/C
Sequence 82, Application US/09451527
Patent No. 6482403
GENERAL INFORMATION:
APPLICANT: Yang, Gek-Kee
APPLICANT: Sim, Gek-Shumlin
APPLICANT: Drelitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/09/451,527
EARLIER FILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 09/322,409
EARLIER FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 82
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
US-09-451-527-82

Alignment Scores:
Pred. No.: 6,03e-93 Length: 610
```



Score:	696.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-787-382-5 (1-134) x US-09-451-527-82 (1-610)

Qy	1	MeArgmetLeuLeuAlaSerLeuLeuAlaLeuGlyAlaAlaIleValSerAlaPhe	20
Db	582	ATGAGAAATGCTTGAATTTGAGTTTGCACTCTGGGGCTGGCTATGTTCTGCTTT	522
Qy	21	AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis	40
Db	522	GCTGTGAAATAATCCCATGAAATAGACTGTGGCAGAGACCTTGACACTGCTCCACATCAT	463
Qy	41	ArgThrThrLeuLeuLeuGlyAsnArgIleAsnLeuMetIleProThrProGluAsnIleAsnHis	60
Db	462	CGAACTTGGCTGATGACGCAATGGAACTCGAATGATTTCTGATCTCGAAAATAAAAAATCAC	403
Qy	61	GlnLeuCyHisIleLeuGluValPheGlnGlyIleAspThrLeuIleAsnGlnThrAlaHis	80
Db	402	CAACTGTGCACTTAAAGAAGTTTTTCAAGGATATAGACACTTGAGAGAACCAAACTGCCAC	343
Qy	81	GlyGluAlaValAspIleLeuPheGlnAsnLeuSerLeuIleLeuGluHisIleGluArg	100
Db	342	GGGAGAGCTGTGATTAACCTATTTCCAAAATCTGTCTTTATATTAAGAACAACATAGAGGC	283
Qy	101	GlnIleLeuLeuArgCysAlaGluGluArgThrPheGluValThrLysPheLeuAspTyrLeuGln	120
Db	282	CAAAAAAAGAGGTGCAGAGAGAAAGATGAGAGTGACAAAGTTCTCTAGACTGACCTGCAA	223
Qy	121	ValPheLeuGlyValIleAsnThrGluTyrPheProGluSer	134
Db	222	GTAATTTCTGTGATATTAACACCGAGTGAACCGGAAAGT	181

RESULT 9  
US-09-371-615A-1

```

Sequence 1, Application US/09371615A
Patent No. 6537781
GENERAL INFORMATION:
APPLICANT: IDEXX LABORATORIES
TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
TITLE OF INVENTION: CANINE INTERLEUKIN 5
FILE REFERENCE: 03604001700DS00
CURRENT APPLICATION NUMBER: US/09/371,615A
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ. ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 405
TYPE: DNA
ORGANISM: Canis familiaris
US-09-371-615A-1

Alignment Scores:
Pred. No.: 6,79e-92 Length: 405
Score: 687.00 Matches: 133
Percent Similarity: 99.25% Conservative: 0
Best Local Similarity: 99.25% Mismatches: 1
Query Match: 98.71% Indels: 0
DB: 4 Gaps: 0

```

US-10-787-382-5 (1-134) x US-09-371-615A-1 (1-405)

Qy 1 MetArGmetLeuLeuLeuLeuSerLeuLeuAlaLeuGlyAlaAlaIrrYValSerLlaPhe 20

Db 1 ATGGAATGGCTTCGAAATTTGAGATTGTGCAGCTCTTGAGGCGCTGCTAAGTTCTGCCTTT 60

Qy 21 AlAlaAlGluAnPProMetAanArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40

Db 61 GCGGTAAATAAATCCCACTGAATAGACGTGGGAGAGAACCTTGACACTCTCTCCACATCAT 120

Oy	41	ArgThrTrpLeuIIGIYAspGIYAsnLeuMetIleProThrProGluAsnIYAsnHis	60
Db	121	CGAACTGGCTGATAGCCGCAATGGAACTGATGATCTCTAAGTAAATAAAAATCAC	180
Oy	61	GInLeuCysIleIYsgIuVaIPhelGInGlyIleAspThrLeuIYsAsnGInThrAlaHis	80
Db	181	CAACTGTGATTAAAGAAAGTTTTCAGGGTTAGACATTGAAAGAACCAAACTGCCAC	240
Oy	81	GIYGIuAlaValAspIYsLeuPheGInAsnLeuSerLeuIleIYsGIuHisIleGIuArg	100
Db	241	GGGGAAGCTGTGATTAACATACTTCCAAACTGTGCTTTTAATAAAGAACATAGAGCGC	300
Oy	101	GInIYsLeuArgCysAlaGIYGIuArgTrpArgValIThrIYsPheLeuAspTrpLeuGIn	120
Db	301	CAAAAAAAGCGTGTGCGAGCAAAAGAGGAGAGTGCACAAAGTTCTTCACTACCTGCAA	360
Oy	121	ValIYsLeuGIYValIleAsnThrGIuTrpThrProGluSer	134
Db	361	GTAATTCCTTGCTGTATTAACACCGAGTGGCAATGGAAGT	402

RESULT 10  
US-09-322-409-85  
; Sequence 85, Application US/09322409

```

UNSUBMITTED ENTREPRENEUR:
APPLICANT: Slim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matchew J.
APPLICANT: Monderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/09/322,409
CURRENT FILING DATE: 1998-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 85
LENGTH: 345
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(345)
US-09-322-409-85

Alignment Scores:
Pred. No.:      1,25e-80
Score:          610.00
Percent Similarity: 100.00%
Best local Similarity: 100.00%
Query Match:    87.64%
DB:              4
Gaps:            0
Length:         345
Matches:        115
Conservative:   0
Mismatch:       0
Indels:         0
Gaps:           0

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US-10-787-382-5 (1-134) x US-09-322-409-85 (1-345)

Qy	20	PheAla1ValAGluAsnProMetAspArgLeuVal11aGluThrLeuThrLeuLeuSerThr	39
Db	1	TTTGCTGTGAAAATCCCATGATGACTGTGGAGAGACCTTGACACGTGCTCCACT	60
Qy	40	HisArgThrTrpLeu11eGlyAspGlyAsnLeuMetC1eProThrProGluAsnLeuAsn	59
Db	61	CATCGAACTGGCTGATAGCGATGCGAAGCTGATGATCTTACTCTGAAAAATAAAAAT	120
Qy	60	HisGlnLeuCys11eIysGluVal1PheGlnGly11eAspThrLeuLeuValAsnGlnThrAla	79
Db	121	CACCAACTGTGCATTAAAGAAAGTTTTCAGCGTATAGACATTGAAGAAACCAAACTGCC	180
Qy	80	HisGlyGluVal1ValAspLeuLeuPheGlnAsnLeuSerLeu11eIysGluHis11eGlu	99
Db	181	CACGGGAGAGCTGTGATTAACCTATTCCTCAAACTGTCTTAAATAAAGAACATAGAG	240

QY 100 ArgGlnLysLysArgCysAlaGlyGluArgTPrpArgValThrLysPheLeuAspTyrLeu 119  
Db 241 CGCCAAAAGAGAGTGTGGAGAGAAAGATGAGAGTGAAGTCTTCTAGACTACTG 300  
QY 120 GlnValPheLeuGlyValIleAsnThrGluTPrpProGluSer 134  
Db 301 CAAGTATTCTTGGTGTATTAACACCGAGTGCACCGGAAAGT 345

RESULT 11  
US-09-322-409-87/c  
Sequence 87, Application US/09322409  
Patent No. 6471957  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Drelitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C1  
CURRENT FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: US/09/322,409  
EARLIER FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 87  
LENGTH: 345  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-09-322-409-87

Alignment Scores:  
Pred. No.: 1,256-80 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 87.64% Indels: 0  
Gaps: 0

US-10-787-382-5 (1-134) x US-09-322-409-87 (1-345)

QY 20 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 39  
Db 345 TTTCCTGTAGAAAATCCCATGATGAGCTGTGGCAGACCTTGACACTGCTCTCCACT 286  
QY 40 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 59  
Db 285 CATGAACCTGGCTGATAGCGGATGAGGAACTGATGATTCTTCTACTCTGAAAATPAAAAAT 226  
QY 60 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 79  
Db 225 CACCAACTGTGCACTTAAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCC 166  
QY 80 HisGlyGluValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 99  
Db 165 CACGGGAGGCTGTGATTAACCTATCCAAAACCTGCTTTAAATAAAGAACACATAGAG 106  
QY 100 ArgGlnLysLysArgCysAlaGlyGluArgTPrpArgValThrLysPheLeuAspTyrLeu 119  
Db 105 CGCCAAAAGAGAGTGTGGAGAGAAAGATGAGAGTGAAGTCTTCTAGACTACTG 46  
QY 120 GlnValPheLeuGlyValIleAsnThrGluTPrpProGluSer 134  
Db 45 CAAGTATTCTTGGTGTATTAACACCGAGTGCACCGGAAAGT 1

RESULT 12  
US-09-451-527-85  
Sequence 85, Application US/09451527  
Patent No. 6482403  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin

APPLICANT: Drelitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C2  
CURRENT FILING DATE: 1999-12-01  
EARLIER APPLICATION NUMBER: US/09/451,527  
EARLIER FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 85  
LENGTH: 345  
TYPE: DNA  
ORGANISM: Canis familiaris  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (1)..(345)  
US-09-451-527-85

Alignment Scores:  
Pred. No.: 1,256-80 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 87.64% Indels: 0  
Gaps: 0

US-10-787-382-5 (1-134) x US-09-451-527-85 (1-345)

QY 20 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 39  
Db 1 TTTCCTGTAGAAAATCCCATGATGAGCTGTGGCAGACCTTGACACTGCTCTCCACT 60  
QY 40 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 59  
Db 61 CATGAACCTGGCTGATAGCGGATGAGGAACTGATGATTCTTCTACTCTGAAAATPAAAAAT 120  
QY 60 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 79  
Db 121 CACCAACTGTGCACTTAAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCC 180  
QY 80 HisGlyGluValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 99  
Db 181 CACGGGAGGCTGTGATTAACCTATCCAAAACCTGCTTTAATAAAGAACACATAGAG 240  
QY 100 ArgGlnLysLysArgCysAlaGlyGluArgTPrpArgValThrLysPheLeuAspTyrLeu 119  
Db 241 CGCCAAAAGAGAGTGTGGAGAGAAAGATGAGAGTGAAGTCTTCTAGACTACTG 300  
QY 120 GlnValPheLeuGlyValIleAsnThrGluTPrpProGluSer 134  
Db 301 CAAGTATTCTTGGTGTATTAACACCGAGTGCACCGGAAAGT 345

RESULT 13  
US-09-451-527-87/c  
Sequence 87, Application US/09451527  
Patent No. 6482403  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Drelitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C2  
CURRENT FILING DATE: 1999-12-01  
EARLIER APPLICATION NUMBER: US/09/451,527  
EARLIER FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306

EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 87  
LENGTH: 345  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-09-451-527-87

Alignment Scores:  
Pred. No.: 1.25e-80 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 87.64% Indels: 0  
DB: 4 Gaps: 0

US-10-787-382-5 (1-134) x US-09-451-527-87 (1-345)

Qy 20 PheAlaValGluAsnProMetAspArgLeuValAlaGluThrLeuLeuSerThr 39  
Db 345 TTGCTGTAGAAATCCCATGATAGACTGTGGAGAGACCTTGACACTGCTCCACT 286

Qy 40 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnGlnThrAla 59  
Db 285 CATGGAATCTGGCTCATAGCGATGGAGACCTGATGATCTTCACTCTGAAAATTAAT 226

Qy 60 HisGlnLeuCybIleGlyGluValPheGlnGlyIleAspThrLeuLeuAsnGlnThrAla 79  
Db 225 CACCAACTGTGATTAAGAAAGTTTTCAGGGTATAGACATTAAGAACCAACTGCC 166

Qy 80 HisGlyGluValAlaAspLeuLeuPheGlnAsnLeuSerLeuIleGlyGluHisGln 99  
Db 165 CACGGGGAGGCTGTGATTAACCTATTCACAACTGTCTTAATTAAGAACCACTAGAG 106

Qy 100 ArgGlnIleAspArgCybAlaGlyGluArgTrpArgValThrLeuPheLeuAspTrpLeu 119  
Db 105 CCCCAAAAAAAGGTGTGCGAGAGAAAGATGAGACGACAAAGTTCTGATCACTG 46

Qy 120 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
Db 45 CAAGTATTCTGTGTATATAACACCGAGTGACACCGGAAAGT 1

RESULT 14  
US-09-079-839-2  
Sequence 2, Application US/09079839  
Patent No. 6048726  
GENERAL INFORMATION:  
APPLICANT: Welman, Joel K.  
TITLE OF INVENTION: INHIBITION OF EOSINOPHILIC INFLAMMATION  
FILE REFERENCE: 09998/002001  
CURRENT APPLICATION NUMBER: US/09/079, 839  
CURRENT FILING DATE: 1998-05-15  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 816  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-079-839-2

Alignment Scores:  
Pred. No.: 1.83e-53 Length: 816  
Score: 430.00 Matches: 87  
Percent Similarity: 77.61% Conservative: 17  
Best Local Similarity: 64.93% Mismatches: 30  
Query Match: 61.78% Indels: 0  
DB: 3 Gaps: 0

US-10-787-382-5 (1-134) x US-09-079-839-2 (1-816)

Qy 1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaLeuValSerAlaPhe 20

Db 45 ATGAGAGATGCTTTCGATTTAGTTGCTAGCTTGGAGCTGCTAGCTATGCCATC 104  
Qy 21 AlaValGluAsnProMetAspArgLeuValAlaGluThrLeuLeuSerThrHis 40  
Db 105 CCCACAGAAATTCACAGAGCATTTGTGAAAGACCTTGCGACCTGCTTCACTCAT 164  
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnGlnThrAlaHis 60  
Db 165 GAACTCTGCTGATAGCAATAGACACTTGAGATTCTGCTTCTTGATCATTAATATAC 224  
Qy 61 GlnLeuCybIleGlyGluValPheGlnGlyIleAspThrLeuLeuAsnGlnThrAlaHis 80  
Db 225 CAACTGTGCACTGAAGAAATCTTTCAGGATATAGACACTGAGAGTCAAACTGTGCA 284  
Qy 81 GlyGluAlaValAlaAspLeuLeuPheGlnAsnLeuSerLeuIleGlyGluHisIleGluArg 100  
Db 285 GGGGGTACTGTGGAAGACTATTCAAAACCTGTCTTAATTAAGAAATATCATTTGACGCGC 344  
Qy 101 GlnIleAspArgCybAlaGlyGluArgTrpArgValThrLeuPheLeuAspTrpLeuGln 120  
Db 345 CAAAAAAGAAAGTGTGAGAAAGAAAGACGAGATTAACCAATTCCTGACTTACCTGCA 404  
Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
Db 405 GAGTTCTGTGTATAGAACACCGAGTGATATAGAAAGT 446

RESULT 15  
US-09-023-655-1236  
Sequence 1236, Application US/09023655  
Patent No. 6607879  
GENERAL INFORMATION:  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: Susan G. Stuart  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESS: INCITE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE: HERewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1236:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 816 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK

CLONE: g288309  
US-09-023-655-1236

Alignment Scores:  
Pred. No.: 1,416-52 Length: 816  
Score: 424.00 Matches: 86  
Percent Similarity: 76.87% Conservative: 17  
Best Local Similarity: 64.18% Mismatches: 31  
Query Match: 60.92% Indels: 0  
DB: 4 Gaps: 0

US-10-787-382-5 (1-134) x US-09-023-655-1236 (1-816)

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QY      1 MetArgMetLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaIYrValSerAlaPhe 20
         |||
Db      45 ATGAGATGCTTTCGACATTTGAGTTTGTAGCTCTTGAGAGCTGCCTAGGTATGCCATC 104
         |||

QY      21 AlaValGluAenProMetAenArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
         |||
Db      105 CCCACAGAAATTCACACAGATGATGTTGTAAGAGACCTTGACACTGCTTCTACTCAT 164
         |||

QY      41 ArgThrTrpLeuIleGlyAaspGlyAenLeuMetIleProThrProGluAenLysAenHis 60
         |||
Db      165 CGAATCTCTGCTGATAGCCAAATGACACTCTGAGATTCCTGTTCTGTACATTAATAATCAC 224
         |||

QY      61 GlnLeuCysIleLysGluValPheGlnGlyIleAapThrLeuLysAenGlnThrAlaHis 80
         |||
Db      225 CAACTGTGCACTGAAGAAATCTTCAAGGAATAGCACACTGAGAGATCAAACTGTGCAA 284
         |||

QY      81 GlyGluAlaValAapLysLeuPheGlnAenLeuSerLeuIleLysGluHisIleGluArg 100
         |||
Db      285 GGGGGTACTGTGGAAGCTATTGAAAACTGTCTTAATAAAGAAATACATTGACGGC 344
         |||

QY      101 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAapLysLeuGln 120
         |||
Db      345 CAAAAAAGAGTGTGAGAAAGAAAGACGAGAGTAAACCAATTCTTAGACTACTGCAA 404
         |||

QY      121 ValPheLeuGlyValIleAenThrGluTrpThrProGluSer 134
         |||
Db      405 GAGTTTCTTGGTGTATGAAACACCGAGTGTGATTAATAGAAAGT 446
         |||

```

Search completed: August 7, 2005, 00:14:16  
Job time : 121.932 secs

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 6, 2005, 22:43:11 ; Search time 556.45 Seconds

(without alignments)  
1561.024 Million cell updates/sec

Title: US-10-787-382-5

Perfect score: 696  
Sequence: 1 MRMLNLSLALGAAVYSAF.....FLDYLYFVLCVINTWTPES 134

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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-LOOPCT=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62  
-TRANS=human40.cdd -LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US10787382 @CGN 1.1 879 @runat\_04082005\_084754\_19405  
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Published Applications NA.\*  
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22: /cgn2\_6/ptodata/2/pubpna/US10I\_NEW\_PUB.seq.\*  
23: /cgn2\_6/ptodata/2/pubpna/US11\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
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26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	100.0	402	9 US-09-755-633-7	Sequence 7, Appl1
2	696	100.0	402	9 US-09-755-633-8	Sequence 8, Appl1
3	696	100.0	402	14 US-10-218-654-83	Sequence 83, Appl1
4	696	100.0	402	14 US-10-218-654-84	Sequence 84, Appl1
5	696	100.0	402	15 US-10-262-439-83	Sequence 84, Appl1
6	696	100.0	402	15 US-10-262-439-84	Sequence 84, Appl1
7	696	100.0	402	19 US-10-787-382-7	Sequence 7, Appl1
8	696	100.0	402	19 US-10-787-382-8	Sequence 7, Appl1
9	696	100.0	610	9 US-09-755-633-4	Sequence 4, Appl1
10	696	100.0	610	9 US-09-755-633-6	Sequence 4, Appl1
11	696	100.0	610	14 US-10-218-654-80	Sequence 80, Appl1
12	696	100.0	610	14 US-10-218-654-82	Sequence 80, Appl1
13	696	100.0	610	15 US-10-262-439-80	Sequence 80, Appl1
14	696	100.0	610	15 US-10-262-439-82	Sequence 82, Appl1
15	696	100.0	610	19 US-10-787-382-4	Sequence 4, Appl1
16	696	100.0	610	19 US-10-787-382-6	Sequence 6, Appl1
17	632.5	90.9	671	9 US-09-755-633-21	Sequence 21, Appl1
18	632.5	90.9	671	19 US-10-787-382-21	Sequence 21, Appl1
19	610	87.6	345	9 US-09-755-633-9	Sequence 9, Appl1
20	610	87.6	345	9 US-09-755-633-11	Sequence 11, Appl1
21	610	87.6	345	14 US-10-218-654-85	Sequence 85, Appl1
22	610	87.6	345	14 US-10-218-654-87	Sequence 87, Appl1
23	610	87.6	345	15 US-10-262-439-85	Sequence 85, Appl1
24	610	87.6	345	15 US-10-262-439-87	Sequence 87, Appl1
25	610	87.6	345	19 US-10-787-382-9	Sequence 9, Appl1
26	610	87.6	345	19 US-10-787-382-11	Sequence 11, Appl1
27	430	61.8	459	22 US-10-880-101A-85	Sequence 85, Appl1
28	430	61.8	816	17 US-10-191-997-90	Sequence 90, Appl1
29	430	61.8	816	21 US-10-929-182-4	Sequence 4, Appl1
30	430	61.8	816	22 US-10-880-101A-87	Sequence 87, Appl1
31	430	61.8	858	16 US-10-295-074-8	Sequence 8, Appl1
32	430	61.8	858	16 US-10-295-074-10	Sequence 10, Appl1
33	430	61.8	858	20 US-10-846-911-8	Sequence 8, Appl1
34	430	61.8	858	20 US-10-846-911-10	Sequence 10, Appl1
35	428	61.5	1658	9 US-09-755-633-19	Sequence 19, Appl1
36	428	61.5	1658	19 US-10-787-382-19	Sequence 19, Appl1
37	424	60.9	816	18 US-10-641-643-1236	Sequence 1236, Ap
38	415.5	59.7	864	16 US-10-295-074-14	Sequence 14, Appl1
39	415.5	59.7	864	20 US-10-846-911-14	Sequence 14, Appl1
40	413.5	59.4	864	16 US-10-295-074-12	Sequence 12, Appl1
41	413.5	59.4	864	20 US-10-846-911-12	Sequence 12, Appl1
42	406.5	58.4	1658	9 US-09-755-633-18	Sequence 18, Appl1
43	406.5	58.4	1658	19 US-10-787-382-18	Sequence 18, Appl1
44	228.5	32.8	3241	22 US-10-880-101A-91	Sequence 91, Appl1
45	222	31.9	6727	9 US-09-800-629A-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-09-755-633-7  
; Sequence 7, Application US/09755633  
; Patent No. US20020127200A1  
GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; RILE REFERENCE: IM-2-C1-C1  
; CURRENT APPLICATION NUMBER: US/09/755,633  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306

Pred. No. is the number of results predicted by chance to have a

;; PRIOR FILING DATE: 1998-05-29  
;; NUMBER OF SEQ ID NOS: 21  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO: 7  
;; LENGTH: 402  
;; TYPE: DNA  
;; ORGANISM: Canis familiaris  
US-09-755-633-7

## Alignment Scores:

Pred. No.:	5,48e-89	Length:	402
Score:	696.00	Matches:	134
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-787-382-5 (1-134) x US-09-755-633-7 (1-402)

Qy 1 MetArgMetLeuAaenLeuSerLeuLeuAlaLeuGlyAlaAlaTYrValSerAlaPhe 20  
Db 1 ATGAGAAATGCTTCTGAATTGAGTTTGCTAGCTCTGGGGCTGCTAATGTTTCTGCCCTT 60  
Qy 21 AlaValGluAaenProMetAaenArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
Db 61 GCTGTAGAAATCCCATGAAATAGACTGTGTGACAGACCTTGACACTGCTCTCCACTCAT 120  
Qy 41 ArgThrTrpLeuIleGlyAaenGlyAaenLeuMetIleProThrProGluAaenLyAaenHis 60  
Db 121 CGAACTTGCTGATAGGCGAATGGAACTTGATGATCTTCTACTCTGAAATTAATAATAC 180  
Qy 61 GluLeuCyrlleYsgIuValPheGlnGlyIleAspThrLeuLyAaenGlnThrAlaHis 80  
Db 181 CAACGTGCATTAAGAAGATTTTCAAGGTATAGACACTTGAAGAAACCAATGCCAC 240  
Qy 81 GlyIuValaValaApyLeuPheGlnAaenLeuSerLeuIleYsgIuHisIleGluArg 100  
Db 241 GGGAGGCTGTGATTAACATATCCAAACTTGCTTAATAAAGAACCATAGAGCGC 300  
Qy 101 GlnLylyAaenGySalagIyGluArgTrpArgValThrLyPheLeuApyTYrLeuGln 120  
Db 301 CAAATAAAGGTGTGCGAGGAAGATGAGAGAGTGAACAAATGTTCTTAGACTTACCTGCA 360  
Qy 121 ValPheLeuGlyValIleAaenThrGluTrpThrProGluSer 134  
Db 361 GTATTCTTGCTGTATATTAACCGAGTGAACCGGAAAGT 402

## RESULT 2

US-09-755-633-8/c  
; Sequence 8, Application US/09755633  
; Patent No. US20020127200A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1-C1  
; CURRENT APPLICATION NUMBER: US/09/755,633  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 8  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-755-633-8

## Alignment Scores:

Pred. No.:	5,48e-89	Length:	402
Score:	696.00	Matches:	134
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-787-382-5 (1-134) x US-09-755-633-8 (1-402)

Qy 1 MetArgMetLeuAaenLeuSerLeuLeuAlaLeuGlyAlaAlaTYrValSerAlaPhe 20  
Db 402 ATGAGAAATGCTTCTGAATTGAGTTTGCTAGCTCTGGGGCTGCTAATGTTTCTGCCCTT 343  
Qy 21 AlaValGluAaenProMetAaenArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
Db 342 GCTGTAGAAATCCCATGAAATAGACTGTGTGACAGACCTTGACACTGCTCTCCACTCAT 263  
Qy 41 ArgThrTrpLeuIleGlyAaenGlyAaenLeuMetIleProThrProGluAaenLyAaenHis 60  
Db 282 CGAACTTGCTGATAGGCGAATGGAACTTGATGATCTTCTACTCTGAAATTAATAATAC 223  
Qy 61 GluLeuCyrlleYsgIuValPheGlnGlyIleAspThrLeuLyAaenGlnThrAlaHis 80  
Db 222 CAACGTGCATTAAGAAGATTTTCAAGGTATAGACACTTGAAGAAACCAATGCCAC 163  
Qy 81 GlyIuValaValaApyLeuPheGlnAaenLeuSerLeuIleYsgIuHisIleGluArg 100  
Db 162 GGGAGGCTGTGATTAACATATCCAAACTTGCTTAATAAAGAACCATAGAGCGC 103  
Qy 101 GlnLylyAaenGySalagIyGluArgTrpArgValThrLyPheLeuApyTYrLeuGln 120  
Db 102 CAAATAAAGGTGTGCGAGGAAGATGAGAGTGAACAAATGTTCTTAGACTTACCTGCA 43  
Qy 121 ValPheLeuGlyValIleAaenThrGluTrpThrProGluSer 134  
Db 42 GTATTCTTGCTGTATATTAACCGAGTGAACCGGAAAGT 1

## RESULT 3

US-10-218-654-83  
; Sequence 83, Application US/10218654  
; Publication No. US20030099609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kea  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 83  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-218-654-83

## Alignment Scores:

Pred. No.:	5,48e-89	Length:	402
Score:	696.00	Matches:	134
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-787-382-5 (1-134) x US-10-218-654-83 (1-402)

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Qy 1 MetArgMetLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaIyValSerAlaPhe 20
Db 1 ATGAGAAATGCTTGGAAATTTGAGTTTGTAGCTCTTGAGGGCTGCTAATGTTTCTGCTTT 60
Qy 21 AlaValGluAenProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
Db 61 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsnHis 60
Db 121 CGAACTGGCTGTAGTAGGCGATGGGAACTGATGATCTTCTACTCTCGAAAATAAAATAC 180
Qy 61 GlnLeuCySileYsgLuvAlaPheGlnGlyIleAspThrLeuLeuYsaenGlnThrAlaHis 80
Db 181 CAACGTGCATTTAAAGAAAGTTTTCAGGGTATAGACATTTGAAACCAACCTGCCAC 240
Qy 81 GlyLuvAlaValAspLysLeuPheGlnAsnLeuSerLeuIleYsgLuvHisIleGluArg 100
Db 241 GGGAGGCTGTGATTAACCTAATTCGAAACCTTGCTTTAATATAAAGAACATAGAGGC 300
Qy 101 GlnLysLysArgCyAlaGlyLuvArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
Db 301 CAAAAAAGAGGTGTGCAGAGAAAGATGAGAGAGTGAACAAAGTTCTTGAAGTACTGCTCA 360
Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
Db 361 GTATTTCTGTGTATTAATTAACCCGAGTGCACCGGAAAGT 402

RESULT 4
US-10-218-654-84/c
; Sequence 84, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Gek-Kee
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218, 654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322, 409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087, 306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-84

Alignment Scores:
Pred. No.: 5.48e-89 Length: 402
Score: 696.00 Matches: 134
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-787-382-5 (1-134) x US-10-218-654-84 (1-402)
Qy 1 MetArgMetLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaIyValSerAlaPhe 20
Db 402 ATGAGAAATGCTTGGAAATTTGAGTTTGTAGCTCTTGAGGGCTGCTAATGTTTCTGCTTT 343
Qy 21 AlaValGluAenProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
Db 342 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsnHis 60
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Db 282 CGAACTGGCTGTAGTAGGCGATGGGAACTGATGATTTCTACTCTCGAAAATAAAATCAC 223
Qy 61 GlnLeuCySileYsgLuvAlaPheGlnGlyIleAspThrLeuLeuYsaenGlnThrAlaHis 80
Db 222 CAACGTGCATTTAAAGAAAGTTTTCAGGGTATAGACATTTGAAACCAACCTGCCAC 163
Qy 81 GlyLuvAlaValAspLysLeuPheGlnAsnLeuSerLeuIleYsgLuvHisIleGluArg 100
Db 162 GGGAGGCTGTGATTAACCTAATTCGAAACCTTGCTTTAATATAAAGAACATAGAGGC 103
Qy 101 GlnLysLysArgCyAlaGlyLuvArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
Db 102 CAAAAAAGAGGTGTGCAGAGAAAGATGAGAGTGAACAAAGTTCTTGAAGTACTGCTCA 43
Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
Db 42 GTATTTCTGTGTATTAATTAACCCGAGTGCACCGGAAAGT 1

RESULT 5
US-10-262-439-83
; Sequence 83, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Gek-Kee
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262, 439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451, 527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322, 409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087, 306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-83

Alignment Scores:
Pred. No.: 5.48e-89 Length: 402
Score: 696.00 Matches: 134
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-787-382-5 (1-134) x US-10-262-439-83 (1-402)
Qy 1 MetArgMetLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaIyValSerAlaPhe 20
Db 1 ATGAGAAATGCTTGGAAATTTGAGTTTGTAGCTCTTGAGGGCTGCTAATGTTTCTGCTTT 60
Qy 21 AlaValGluAenProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
Db 61 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsnHis 60
Db 61 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
Qy 61 GlnLeuCySileYsgLuvAlaPheGlnGlyIleAspThrLeuLeuYsaenGlnThrAlaHis 80
Db 121 CGAACTGGCTGTAGTAGGCGATGGGAACTGATGATCTTCTACTCTCGAAAATAAAATAC 180
Qy 81 GlnLeuCySileYsgLuvAlaPheGlnGlyIleAspThrLeuLeuYsaenGlnThrAlaHis 80
Db 181 CAACGTGCATTTAAAGAAAGTTTTCAGGGTATAGACATTTGAAACCAACCTGCCAC 240
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Oy	81	G G L A A A V A L S P Y S E U P H E G I N E N S E U L I E Y G I N H A I E G I N A T G	100
Db	241	G G G A G C G T G G A T A A C T A T T C A A A C T G T C T T A A T A A A G A C A T A G A C G C	300
Oy	101	G L L Y S Y R A T G C S A I A G I G I U A T G T P R A G V A L T h t l y S P h e L e A S P T Y r L e U n	120
Db	301	C A A A A A A A A G G T G C G G A G A A G A T G A A G A G G A A G T C T A G A C T A C T G C A	360
Oy	121	V A I P h e U c I V A I I L e A n T h r g I U T P T h r P r o G i U S e r	134
Db	361	G T A T T T C T G T G T A T A T A A C C G A G T G A C C G G A A G T	402

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RESULT 6
US-10-262-439-84/C
: Sequence 84, Application US/10262439
: Publication No. US20030143196A1
: GENERAL INFORMATION:
: APPLICANT: Sim, Gek-Kee
: APPLICANT: Yang, Shumin
: APPLICANT: Dreitz, Matthew J.
: APPLICANT: Wonderling, Ramani S.
: TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
: FILE REFERENCE: IM-2-C2
: CURRENT APPLICATION NUMBER: US/10/262,439
: CURRENT FILING DATE: 2002-09-30
: PRIOR APPLICATION NUMBER: US/09/451,527
: PRIOR FILING DATE: 1999-12-01
: PRIOR APPLICATION NUMBER: 09/322,409
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/087,306
: PRIOR FILING DATE: 1998-05-29
: NUMBER OF SEQ ID NOS: 1/4
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 84
: LENGTH: 402
: TYPE: DNA
: ORGANISM: Canis familiaris
US-10-262-439-84

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Alignment Scores:	
Pred. No.:	5,48e-89
Score:	996.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	15
US-10-787-382-5 (1-134) x US-10-262-439-84 (1-402)	
Length:	402
Matches:	134
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

Qy	1	MetArgMetLeuLeuLeuLeuSerLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerSerAlaPhe	20
Ds	402	ATGAGAAATGCTCTCGAAATTTGAGTTTGCTAGCTCTTGAGCGCTGAGCTTAATGTTTCTGCGCTTT	343
Qy	21	AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerSerThrHis	40
Ds	342	GCTGTAGAAAATTCCTCAATGAAATAGACTGGTGGGAGAGACCTTGACACTGCTCTCCACTCAT	283
Qy	41	ArgThrTrpLeuIleGlyAsnArgIleAsnLeuMetIleProThrProGluAsnIleAsnHis	60
Ds	282	CGAACTTGGCTGATAGCGCATGGGAACTCGATGATTCCTCACTCGTGAATAATGAAAATTCAC	223
Qy	61	GlnLeuCybIleLeuGluValPheGlnGlyIleAspThrLeuIleValMetGlnThrAlaHis	80
Ds	222	CAACTGTGCATTTAAAGAAAGTTTTCAGGGTATAGACACTGGAAGAACCAAACTGCCAC	163
Qy	81	GlyGlnIleValIleAspIleLeuPheGlnAsnLeuSerLeuIleLeuGluHisIleLeuGluArg	100
Ds	162	GGGGAGGCTGTGGATTAACCTATTCACAAACTGTCTTTAATTAAGAAACAATAGAACGC	103
Qy	101	GlnIleValIleArgCybAlaGlyGluArgTyrPAspValIleThrIlePheLeuAspTyrLeuGln	120
Ds	102	CAAAAATAAAGGTGTGCGAGAGAAATAGAGAGGTGACAAAGTCTCTAGACTTACTCGAA	43

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Oy      121 ValPheLeuGlyValIleasnThrGluTyrThrProGluSer 134
         |||||
Db      42 GTATTCTTGGTGTAATAACACCGAGTGACACCGAAAGT 1

```

```

RESULT 7
US-10-787-382-7
: Sequence 7, Application US/10787382
: Publication No. US20040191868A1
: GENERAL INFORMATION:
: APPLICANT: Yang, Shumin
: APPLICANT: McCall, Catherine A.
: TITLE OF INVENTION: WEBER, ERIC R.
: TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
: FILE REFERENCE: IM-2-C1-C1
: CURRENT APPLICATION NUMBER: US/10/787,382
: CURRENT FILING DATE: 2004-02-24
: PRIOR APPLICATION NUMBER: US/09/755,633
: PRIOR FILING DATE: 2001-01-05
: PRIOR APPLICATION NUMBER: 09/322,409
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/087,306
: PRIOR FILING DATE: 1998-05-29
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 7
: LENGTH: 402
: TYPE: DNA
: ORGANISM: Canis familiaris
US-10-787-382-7

```

Alignment Scores:	
Pred. No.:	5, 48e-89
Score:	696.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	19
Length:	4
Matches:	4
Conservative:	1
Mismatches:	0
Indels:	0
Gaps:	0

US-10-787-382-5 (1-134) X US-10-787-382-7 (1-402)

Qy	1	MetArgMetLeuLeuLeuLeuSerLeuLeuLeuLeuGlyAlaAlaGlyValSerPhe	20
Db	1	ATAGAGATGCTTCTGATTAATTGAGTTTGCTAGCTCTTGAGGAGCTGGCTTAAGTTTCTGCCTTT	60
Qy	21	AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis	40
Db	61	GCCTGAGAAAATCCCATGAAATGAACTGGAGGCAAGAACTTGACACCTGCTCCATCAT	120
Qy	41	ArgThrTyrLeuLeuLeuGlyAspGlyValenLeuMetLeuProThrProGluAsnIleAsnHis	60
Db	121	CGAACTGGCTGATAGGCGCATGGAACTGTGATGATTTCTACTCTCGAAAAATAAAAATCAC	180
Qy	61	GlnLeuCysIleLeuGluValPheGlnGlyIleAspThrLeuLeuAsnGlnThrAlaHis	80
Db	181	CAACTGTGCATTAAAGAAAGTTTTTCAAGGTTATAGCACTTGAAAGAACCAAACTGCCAC	240
Qy	81	GlyGluAlaValAspIleLeuPheGlnAsnLeuSerLeuIleGlyGluHisIleGluArg	100
Db	241	GGGAGAGCTGTGGATTAACTATTCCAAAACTTGCTTTAAATAAAGAACCATGTAGACGC	300
Qy	101	GlnLeuLeuArgCysAlaGlyGluArgGlyTrpArgValThrIlePheLeuAspTyrLeuGln	120
Db	301	CAAAAAAAGGTGTGCAGAGAAAGATGAGAGTGAACAAAGTTCTTGNACTACTGCA	360
Qy	121	ValPheLeuGlyValIleAsnThrGluThrProGluSer	134
Db	361	GTAATTCCTGTGTATAAACAACGATGGACACCGGAAAGT	402

RESULT 8  
 US-10-787-382-8/C  
 ; Sequence 8, Application US/10787382



Publication No. US20040191868A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Shumin  
APPLICANT: McCall, Catherine A.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C1-C1  
CURRENT APPLICATION NUMBER: US/10/787,382  
CURRENT FILING DATE: 2004-02-24  
PRIOR APPLICATION NUMBER: US/09/755,633  
PRIOR FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 402  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-10-787-382-8

Alignment Scores:  
Pred. No.: 5,486-89 Length: 402  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 19 Gaps: 0

US-10-787-382-5 (1-134) x US-10-787-382-8 (1-402)

QY 1 MetArgMetLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20  
DB 402 ATGAGAAATGCTTGAATTTGAGTTTGCTAGCTCTGGGGCTGGCTATGTTTCCCTTT 343  
QY 21 AlaValGluAenPrometAenArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
DB 342 GCTTGAAGAAATCCCATGAATGACTGTGGCAGAGACCTTGACACTGCTCCACTCAT 283  
QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60  
DB 282 CGAAGTGGCTGATAGGCGATGGAGACTGATGATCTTCACTCTGAAAATTAATAATAC 223  
QY 61 GlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80  
DB 222 CAACGTGCATTTAAAGAAAGTTTTCAGGGTATAGCACTTGAAGAACCAAACTGCCAC 163  
QY 81 GlyGluAlaValAlaPylsLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100  
DB 162 GGGAGGCTGTGATTAACATACTTCCAAAATGCTTTAATAAAGAACACATAGAGCGC 103  
QY 101 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120  
DB 102 CAAAAAAGAGTGTGCAGAGAAAGATGAGAGTGAAGAAAGTTCTTAGACTACTGCA 43  
QY 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
DB 42 GTATTTCTGTGTATTAACACCGAGTGCACCGGAAAGT 1

RESULT 9  
US-09-755-633-4  
Sequence 4, Application US/09755633  
Patent No. US20020127200A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Shumin  
APPLICANT: McCall, Catherine A.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C1-C1

CURRENT APPLICATION NUMBER: US/09/755,633  
CURRENT FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 610  
TYPE: DNA  
ORGANISM: Canis familiaris  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (29) .. (430)  
US-09-755-633-4

Alignment Scores:  
Pred. No.: 1,036-88 Length: 610  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-787-382-5 (1-134) x US-09-755-633-4 (1-610)

QY 1 MetArgMetLeuLeuAenLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20  
DB 29 ATGAGAAATGCTTGAATTTGAGTTTGCTAGCTCTGGGGCTGGCTATGTTTCCCTTT 88  
QY 21 AlaValGluAenPrometAenArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
DB 89 GCTTGAAGAAATCCCATGAATGACTGTGGCAGAGACCTTGACACTGCTCCACTCAT 148  
QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60  
DB 149 CGAAGTGGCTGATAGGCGATGGAGACTGATGATCTTCACTCTGAAAATTAATAATAC 208  
QY 61 GlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80  
DB 209 CAACGTGCATTTAAAGAAAGTTTTCAGGGTATAGCACTTGAAGAACCAAACTGCCAC 268  
QY 81 GlyGluAlaValAlaPylsLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100  
DB 269 GGGAGGCTGTGATTAACATACTTCCAAAATGCTTTAATAAAGAACACATAGAGCGC 328  
QY 101 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120  
DB 329 CAAAAAAGAGTGTGCAGAGAAAGATGAGAGTGAAGAAAGTTCTTAGACTACTGCA 388  
QY 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
DB 389 GTATTTCTGTGTATTAACACCGAGTGCACCGGAAAGT 430

RESULT 10  
US-09-755-633-6/C  
Sequence 6, Application US/09755633  
Patent No. US20020127200A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Shumin  
APPLICANT: McCall, Catherine A.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C1-C1  
CURRENT APPLICATION NUMBER: US/09/755,633  
CURRENT FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 21

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 610  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-09-755-633-6

Alignment Scores:  
Pred. No.: 1,03e-88 Length: 610  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-787-382-5 (1-134) X US-09-755-633-6 (1-610)

QY 1 MetArgMetLeuLeuLeuSerLeuLeuAlaLeuGlyAlaAlaIleValSerAlaPhe 20  
DB 582 ATGAGAAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCTATGTTTCTGCTTT 523  
QY 21 AlaValGluAspProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40  
DB 522 GCTGTAGAAAATCCCATGAATAGACTGTGACAGAACCTTGACACTGCTCTCCACTCAT 463  
QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleAsnHis 60  
DB 462 CGAAGCTTGCTGATAGCGCATGGGAACCTGATGATTCCTGCTGAAAAATCAAC 403  
QY 61 GluLeuCyS1leuGlyValPheGlnGlyIleAspThrLeuIleuAsnGlnThrAlaHis 80  
DB 402 CAACGTGCACTTAAAGAAAGTTTTCAGGCTATAGACACATTGAAGAACCAAACTGCCAC 343  
QY 81 G1G1uAlaValAlaAspIleuPheGlnAsnLeuSerLeuIleuGlyHisIleGluArg 100  
DB 342 GGGAGGCTGTGATTAACATTCCTCAAACTTGTCTTATTAAGAACACATAGAGCC 283  
QY 101 GlnIleuAsnArgCyS1leuGlyValArgTrpArgValThrIleuPheLeuAspIleuGln 120  
DB 282 CAATAAAAAAGGTGTGACGAGGAAAGATGAGAGTGAACAAAGTCTTACACTACCTCAA 223  
QY 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
DB 222 GTATTCTTGTTGTTAATAAACACCGAGTGAACCGGAAAGT 181

## RESULT 11

US-10-218-654-80  
Sequence 80, Application US/10218654  
Publication No. US20030099609A1  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Drelitz, Matthew J.  
APPLICANT: Wondertling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C1  
CURRENT APPLICATION NUMBER: US/10/218,654  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: US/09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 80  
LENGTH: 610  
TYPE: DNA  
ORGANISM: Canis familiaris  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (25)..(430)  
US-10-218-654-80

## Alignment Scores:

Pred. No.: 1,03e-88 Length: 610  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-787-382-5 (1-134) X US-10-218-654-80 (1-610)

QY 1 MetArgMetLeuLeuLeuSerLeuLeuAlaLeuGlyAlaAlaIleValSerAlaPhe 20  
DB 29 ATGAGAAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCTATGTTTCTGCTTT 88  
QY 21 AlaValGluAspProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40  
DB 89 GCTGTAGAAAATCCCATGAATAGACTGTGACAGAACCTTGACACTGCTCTCCACTCAT 148  
QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleAsnHis 60  
DB 149 CGAAGCTTGCTGATAGCGCATGGGAACCTGATGATTCCTGCTGAAAAATCAAC 208  
QY 61 GluLeuCyS1leuGlyValPheGlnGlyIleAspThrLeuIleuAsnGlnThrAlaHis 80  
DB 209 CAACGTGCACTTAAAGAAAGTTTTCAGGCTATAGACACATTGAAGAACCAAACTGCCAC 268  
QY 81 G1G1uAlaValAlaAspIleuPheGlnAsnLeuSerLeuIleuGlyHisIleGluArg 100  
DB 269 GGGAGGCTGTGATTAACATTCCTCAAACTTGTCTTATTAAGAACACATAGAGCC 328  
QY 101 GlnIleuAsnArgCyS1leuGlyValArgTrpArgValThrIleuPheLeuAspIleuGln 120  
DB 329 CAATAAAAAAGGTGTGACGAGGAAAGATGAGAGTGAACAAAGTCTTACACTACCTCAA 388  
QY 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
DB 389 GTATTCTTGTTGTTAATAAACACCGAGTGAACCGGAAAGT 430

## RESULT 12

US-10-218-654-82/C  
Sequence 82, Application US/10218654  
Publication No. US20030099609A1  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Drelitz, Matthew J.  
APPLICANT: Wondertling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C1  
CURRENT APPLICATION NUMBER: US/10/218,654  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: US/09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 82  
LENGTH: 610  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-10-218-654-82

## Alignment Scores:

Pred. No.: 1,03e-88 Length: 610  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-787-382-5 (1-134) x US-10-218-654-82 (1-610)

QY 1 MetArgMetLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaATYValSerAlaPhe 20  
Db 582 ATGGAATGCTTCGAAATTTAGATTGCTACCTCTGGGCTGCTATGTTCTGCCCTT 523  
QY 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
Db 522 GCTGTAGAAATCCCATTAATAGACTGTGCGACAGACTTGACACTGCTCTCCACTCAT 463  
QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60  
Db 462 CGAAGTGGCTGATAGGCGATGGGAACTGATGATTCCTACTCTCGAAATTAATAATCAC 403  
QY 61 GlnLeuGlyIleLeuGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80  
Db 402 CAATGGCATTAAGAAGATTTCAGGGTATAGACATTAAGAACCAATGCCAC 343  
QY 81 GlyGluAlaValAlaPheLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100  
Db 342 GGGAGGCTGTGATTAACCTATTCCTCAAACTGCTTTAATTAAGAACAATAGAGCGC 283  
QY 101 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120  
Db 282 CAAAAAAGAGTGTGACAGAAAGATGAGAGTGAACAAGTTCCTAGACTACCTGCA 223  
QY 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
Db 222 GTATTCTTGTTGATTAACACCGAGTGAACCGGAAGT 181

## RESULT 13

US-10-262-439-80  
; Sequence 80, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kea  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; PRIOR FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 80  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29)..(430)  
US-10-262-439-80

## Alignment Scores:

Pred. No.: 1,03e-88 Length: 610  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 15 Gaps: 0

US-10-787-382-5 (1-134) x US-10-262-439-80 (1-610)

QY 1 MetArgMetLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaATYValSerAlaPhe 20  
|||||

Db 29 ATGAAGATGCTTCGAAATTTAGATTGCTAGCTCTGGGCTGCTATGTTCTGCCCTT 88

QY 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
Db 89 GCTGTAGAAATCCCATTAATAGACTGTGCGACAGACTTGACACTGCTCTCCACTCAT 148  
QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60  
Db 149 CGAAGTGGCTGATAGGCGATGGGAACTGATGATTCCTACTCTCGAAATTAATAATCAC 208  
QY 61 GlnLeuGlyIleLeuGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80  
Db 209 CAATGGCATTAAGAAGATTTCAGGGTATAGACATTAAGAACCAATGCCAC 268  
QY 81 GlyGluAlaValAlaPheLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100  
Db 269 GGGAGGCTGTGATTAACCTATTCCTCAAACTGCTTTAATTAAGAACAATAGAGCGC 328  
QY 101 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120  
Db 329 CAAAAAAGAGTGTGACAGAAAGATGAGAGTGAACAAGTTCCTAGACTACCTGCA 388  
QY 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
Db 389 GTATTCTTGTTGATTAACACCGAGTGAACCGGAAGT 430

## RESULT 14

US-10-262-439-82/c  
; Sequence 82, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kea  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; PRIOR FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 82  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-262-439-82

## Alignment Scores:

Pred. No.: 1,03e-88 Length: 610  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 15 Gaps: 0

US-10-787-382-5 (1-134) x US-10-262-439-82 (1-610)

QY 1 MetArgMetLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaATYValSerAlaPhe 20  
Db 582 ATGGAATGCTTCGAAATTTAGATTGCTACCTCTGGGCTGCTATGTTCTGCCCTT 523  
QY 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
Db 522 GCTGTAGAAATCCCATTAATAGACTGTGCGACAGACTTGACACTGCTCTCCACTCAT 463  
QY 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60  
|||||

Db 462 CGAAGCTGGCTGATAGGCGATGGAGACCTGATGATCTCTACTCTCGAAAAATTAATCAAC 403  
Qy 61 Glnleucysrllelysglvalipheglnglyrlleapthrlleuysannglntthlalihs 80  
Db 402 CAACTGGCATTAAGAAGTTTTCAGGGTATAGACATTAAGAAACCAACTGGCCAC 343  
Qy 81 G1yglualavalaaplyslleupheglasnlleuSerleuilelysgluhlsilegluarg 100  
Db 342 GGGGAGGCTGTGATTAACCTATTCCTTAATTAAGAAACATAGAGCGC 283  
Qy 101 GlnlyslsargCysalaglgluargtrpargvalthrlyspheleuaptryleugln 120  
Db 282 CAAAAAAGGTGTGAGGAGAAAGATGGAGGTGACAAAGTTCCTTAGACTACGTCAA 223  
Qy 121 ValpheuglyvalilleaenthrgluttrpThrProgluser 134  
Db 222 GTATTCTTGSTGTATTAACACCGAGTGCACCGGAAAGT 181

RESULT 15  
US-10-787-382-4  
Sequence 4, Application US/10787382  
Publication No. US20040191868A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Shumin  
APPLICANT: McCall, Catherine A.  
APPLICANT: Weber, Eric R.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C1-C1  
CURRENT APPLICATION NUMBER: US/10/787,382  
PRIOR FILING DATE: 2004-02-24  
PRIOR APPLICATION NUMBER: US/09/755,633  
PRIOR FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 610  
TYPE: DNA  
ORGANISM: Canis familiaris  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (29)..(430)  
US-10-787-382-4

Alignment Scores:  
Pred. No.: 1.03e-88 Length: 610  
Score: 696.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 19 Gaps: 0

US-10-787-382-5 (1-134) x US-10-787-382-4 (1-610)

Qy 1 MetlrghtleuLeuAenSerleuLeuAlaleuglyalaaatyvalserlaph 20  
Db 29 ATGAGAAATGCTTCGAAATTTAGATTGCTAGCTCTGGGCTGCTATGTTCTGCCCTT 88  
Qy 21 Alaya1gluaenPrometAsnArgleuValalaglthrleuthrlleuSerThrHis 40  
Db 89 GCTGTAGAAATCCCATATAGACTGTGTGGCAGAGACTTGACCTGCTCCATCAT 148  
Qy 41 ArgThrTrpLeuileglyAspGlyAsnleuMetileProthrProgluasnllyAsnHis 60  
Db 149 CGAAGCTGGCTGATAGGCGATGGAACTGATGATTCCTACTCGGAAAAATTAATCAAC 208  
Qy 61 Glnleucysrllelysglvalipheglnglyrlleapthrlleuysannglntthlalihs 80

Db 209 CAACTGCAATTAAAGAGTTTTCAGGGTATAGACATTAAGAAACCAACTGCCAC 268  
Qy 81 G1yglualavalaaplyslleupheglasnlleuSerleuilelysgluhlsilegluarg 100  
Db 269 GGGGAGGCTGTGATTAACCTATTCCTTAATTAAGAAACATAGAGCGC 328  
Qy 101 GlnlyslsargCysalaglgluargtrpargvalthrlyspheleuaptryleugln 120  
Db 329 CAAAAAAGGTGTGAGGAGAAAGATGGAGGTGACAAAGTTCCTTAGACTACGTCAA 388  
Qy 121 ValpheuglyvalilleaenthrgluttrpThrProgluser 134  
Db 389 GTATTCTTGSTGTATTAACACCGAGTGCACCGGAAAGT 430

Search completed: August 7, 2005, 03:15:59  
Job time : 559.45 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus2 model

Run on: August 6, 2005, 19:45:30 ; Search time 2814 Seconds

(without alignments)  
1812.584 Million cell updates/sec

Title: US-10-787-382-5

Perfect score: 696

Sequence: 1 MRMLNLSLALGAAVYSAF.....FLDYLYPFLGVINTEWTPES 134

Scoring table:

BLASTN62	
Xgapop 10.0 , Xgapext 0.5	
Xgapop 10.0 , Ygapext 0.5	
Ygapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 34239544 segs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool\_p/US10787382/runat\_04082005\_084752\_19305/app\_query.fasta\_1.590  
-DB=EST -QMT=fastcap -SUFFIX=rev -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USR=US10787382\_@CGN\_1\_1\_6628\_@runat\_04082005\_084752\_19305 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEODRPRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_g981:\*  
9: gb\_g982:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	430	61.8	405	9	AY412020 Homo sapi
2	430	61.8	456	6	CD559532 AGENCOURT
3	430	61.8	456	6	CD559532 AGENCOURT
4	430	61.8	470	6	CD559687 AGENCOURT
5	430	61.8	492	6	CD559533 AGENCOURT
6	417	59.9	458	3	BC066279 Homo sapi
7	417	59.9	463	6	BC066280 Homo sapi
8	417	59.9	463	6	CD559535 AGENCOURT
9	417	59.9	467	6	CD559690 AGENCOURT

C	10	417	59.9	472	6	CD559689	CD559689 AGENCOURT
C	11	417	59.9	489	6	CD559536	CD559536 AGENCOURT
C	12	417	59.9	817	3	BC066137	BC066137 Homo sapi
C	13	411	59.1	405	9	AY412021	AY412021 Pan trogl
C	14	406	58.3	456	3	BC066281	BC066281 Homo sapi
C	15	406	58.3	467	6	CD559688	CD559688 AGENCOURT
C	16	406	58.3	478	6	CD559534	CD559534 AGENCOURT
C	17	383	55.0	477	6	CD559608	CD559608 AGENCOURT
C	18	356.5	51.2	622	9	CR311159	CR311159 tigr-g88
C	19	336	48.3	399	9	AY412022	AY412022 Mus muscu
C	20	186	26.7	781	9	CR235404	CR235404 Reverse B
C	21	165	23.7	503	5	BQ598873	BQ598873 MI-P-E4-a
C	22	129	18.5	495	7	CR554944	CR554944 M42P469N
C	23	94.5	13.6	737	9	CR026247	CR026247 Reverse s
C	24	91.5	13.1	811	4	BT247887	BT247887 602959820
C	25	88.5	12.7	681	6	CD894793	CD894793 G118.127C
C	26	86	12.4	412	5	BM573727	BM573727 BM573727
C	27	84	12.1	496	1	AA689677	AA689677 v803C02.x
C	28	83.5	12.0	1038	5	BU198659	BU198659 DCBCKG01
C	29	81.5	11.7	703	9	CL301640	CL301640 gba2 CH25
C	30	81.5	11.7	769	5	BU227588	BU227588 603800631
C	31	81.5	11.7	772	7	CR234700	CR234700 PtdA07001
C	32	81	11.6	1267	3	CR727373	CR727373 Tetracton
C	33	80.5	11.6	518	4	BM284184	BM284184 k131b02.y
C	34	80.5	11.6	589	6	CD305286	CD305286 StrPu691.
C	35	79.5	11.4	618	2	BE920538	BE920538 EST424307
C	36	79.5	11.4	642	8	BH009635	BH009635 e31C06.x
C	37	79.5	11.4	675	4	B1561257	B1561257 603256408
C	38	79	11.4	425	2	AW068198	AW068198 cn23C07.y
C	39	79	11.4	504	6	CB047608	CB047608 NISC_5903
C	40	79	11.4	560	1	AJ745225	AJ745225 AJ745225
C	41	79	11.4	606	7	CO896018	CO896018 BoyGen.24
C	42	79	11.4	607	5	BQ018244	BQ018244 UI-H-DH1
C	43	79	11.4	644	6	CB047607	CB047607 NISC_5903
C	44	79	11.4	660	7	CN371286	CN371286 170006000
C	45	79	11.4	666	6	CA311187	CA311187 UI-CF-PN0

#### ALIGNMENTS

RESULT 1	AY412020	405 bp	DNA	linear	GSS 16-DEC-2003
LOCUS	AY412020				
DEFINITION	Homo sapiens IUS gene, VIRUTAL TRANSCRIPT, partial sequence.				
ACCESSION	AY412020				
VERSION	AY412020.1	GI:39767985			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 405) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
REFERENCE	PUBMED 14671302				
AUTHORS	2 (bases 1 to 405) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
source	1. .405				

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## ORIGIN

## Alignment Scores:

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Score:	430.00	Matches:	87
Percent Similarity:	77.61%	Conservative:	17
Best Local Similarity:	64.93%	Mismatches:	30
Query Match:	61.78%	Indels:	0
DB:	9	Gaps:	0

US-10-787-382-5 (1-134) x AY412020 (1-405)

Qy 1 MetArgMetLeuLeuAanLeuSerLeuLeuAlaLeuGlyAlaAlaTyValSerAlaPhe 20

Db 1 ATGAGAGATGCTTGTGCAATTTGAGTTGCTTACTGCTTGGAGCTGCTACGTATGCCATC 60

Qy 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40

Db 61 CCCACAGAAATTCACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120

Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleAsnHis 60

Db 121 GGAATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180

Qy 61 GlnLeuCyIleLeuGluValAlaPheGlnGlyIleAsnThrLeuLeuValAsnGlnThrAlaHis 80

Db 181 CAACGTGACACTGAGAAATCTTTCAGGAGATGACACACTGAGAGATCAAACTGTGCAA 240

Qy 81 GlyIleValAlaValAspLeuPheGlnAsnLeuSerLeuIleGlyHisIleGluArg 100

Db 241 GGGGGTACTGTGAAGAAGCTATTAACAACTGCTTAATAAAGAAATACATTAAGAGCC 300

Qy 101 GlnIleValAspArgCysAlaGlyIleGluArgTrpArgValThrIlePheLeuAspTyIleGln 120

Db 301 CAAATAAATAAGTGTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAATTCCTAGACTTACTGCA 360

Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134

Db 361 GAGTTTCTGTGTATATGACACCGAGTGATATATAGAAAGT 402

RESULT 2

CD559532 456 bp mRNA linear EST 11-JUN-2003

LOCUS AGENCOURT\_14497057 NIH\_MGC\_195 Homo sapiens cDNA clone

DEFINITION IMAGE:6971772 5', mRNA sequence.

ACCESSION CD559532

VERSION CD559532.1 GI:31585600

KEYWORDS EST.

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 456)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLES National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgsapbs-remail.nih.gov  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: Bhat Laboratory  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/MLML at:

http://image.llnl.gov  
Plate: IRBK1 row: 9 column: 11  
High quality sequence stop: 456.  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
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/issue\_type="mixed"  
/lab\_host="DH5A (TI phage-resistant)"  
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/note="Vector: pDNR-Dual1; Site 1: loxp-Sall; Site 2:  
loxP-HindIII; Clones from this library have been  
PCR-amplified using gene-specific primers to confirm the  
complete open reading frame (based on known gene sequences  
available from NCBI's RefSeq). Template for PCR is cDNA  
derived from either pooled cytoplasmic polyA RNA from 30  
cells lines or pooled total RNA from 10 different tissues  
(from BD Biosciences/Clontech and Washington University).  
PCR products are directionally cloned into the loxp sites  
of the pDNR-Dual vector. Library constructed by Dr.  
Narayan Bhat, Bart Bere and Hongling Liao (Gene  
Expression Laboratory, Research Technology Program, SAIC  
Frederick, NCI-Frederick, Frederick, MD 21702). For  
information on which gene each clone represents, please  
visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearrayed\_plates/IRBK\_prev.dat  
a Note: this is a NIH\_MGC library."

## FEATURES

## source

## ORIGIN

## Alignment Scores:

Pred. No.:	1.69e-44	Length:	456
Score:	430.00	Matches:	87
Percent Similarity:	77.61%	Conservative:	17
Best Local Similarity:	64.93%	Mismatches:	30
Query Match:	61.78%	Indels:	0
DB:	6	Gaps:	0

US-10-787-382-5 (1-134) x CD559532 (1-456)

Qy 1 MetArgMetLeuLeuAanLeuSerLeuLeuAlaLeuGlyAlaAlaTyValSerAlaPhe 20

Db 22 ATGAGAGATGCTTGTGCAATTTGAGTTGCTTACTGCTTGGAGCTGCTACGTATGCCATC 81

Qy 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40

Db 82 CCCACAGAAATTCACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 141

Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleAsnHis 60

Db 142 GGAATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 201

Qy 61 GlnLeuCyIleLeuGluValAlaPheGlnGlyIleAsnThrLeuLeuValAsnGlnThrAlaHis 80

Db 202 CAACGTGACACTGAGAAATCTTTCAGGAGATGACACACTGAGAGATCAAACTGTGCAA 261

Qy 81 GlyIleValAlaValAspLeuPheGlnAsnLeuSerLeuIleGlyHisIleGluArg 100

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Qy 101 GlnIleValAspArgCysAlaGlyIleGluArgTrpArgValThrIlePheLeuAspTyIleGln 120

Db 322 CAAATAAATAAGTGTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAATTCCTAGACTTACTGCA 381

Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134

Db 382 GAGTTTCTGTGTATATGACACCGAGTGATATATAGAAAGT 423

RESULT 3

CD559686/c 456 bp mRNA linear EST 11-JUN-2003

LOCUS AGENCOURT\_14497093 NIH\_MGC\_195 Homo sapiens cDNA clone

DEFINITION

IMAGE:6971772.3', mRNA sequence.

ACCESSION CD559686  
 VERSION CD559686.1 GI:31585754  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 456)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Narayan Bhat  
 CDNA Library Preparation: Bhat Laboratory  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 plate: IRBK1 row: 9 column: 11  
 High quality sequence stop: 456.

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 /clone\_id="NIH\_MGC\_195"  
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 A Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	1.69e-44	Length:	456
Score:	430.00	Matches:	87
Percent Similarity:	77.61%	Conservative:	17
Best Local Similarity:	64.93%	Mismatches:	30
Query Match:	61.78%	Indels:	0
DB:	6	Gaps:	0

US-10-787-382-5 (1-134) x CD559686 (1-456)

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 Db 433 ATGAGATGCTTGCATTGAGTTGCTTGTGAGCTGCTACGTATGATCCATC 374  
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 QY 41 ArGThrTrpLeuIlEgLYaSPGLYAsnLeuWetIlEPrOThrProGLuaSnLYaSnHis 60  
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 QY 61 GlnLeuCyAlleYsGluValPheGlnGlyTlleApThrLeuLYaSnGlnThrAlaHis 80  
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 Db 253 CAACCTGCACTGAAGAAATCTTTCAGGAAATAGCACACGAGAGCAAACTGTGCA 194  
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 Db 73 GAGTTCTTGCTGTATGAACACCGAGTGAATATAGAAAGT 32  
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RESULT 4  
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 LOCUS 470 bp mRNA linear EST 19-NOV-2003  
 DEFINITION AGENCOURT\_14497029 NIH\_MGC\_195 Homo sapiens cDNA clone  
 IMAGE:6971771.5', mRNA sequence.

ACCESSION CD559687  
 VERSION CD559687.2 GI:38453484  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 470)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 On Jun 10, 2003 this sequence version replaced gi:31585755.  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Narayan Bhat  
 CDNA Library Preparation: Bhat Laboratory  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 plate: IRBK1 row: 9 column: 10  
 High quality sequence start: 14  
 High quality sequence stop: 470.

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information on which gene each clone represents, please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearranged\_plates/IRBK.presv.dat  
a Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.:	1.76e-44	Length:	470
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Query Match:	61.78%	Indels:	0
DB:	6	Gaps:	0

US-10-787-382-5 (1-134) x CD55953 (1-470)

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Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAenLysAsnHis 60
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Qy 61 GluLeuCyAlleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80
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Db 206 GGGGGTACTGTGAAAGACTATTCAAAATCTTCTTAATAAAGAAATACATGACGCC 147
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Qy 101 GlnLysLysArgCyAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
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Db 146 CAAATAAAGAGTGTGAGAGAAAGACGAGAGATTAACCAATTCCTAGACTACTGCAA 87
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DEFINITION IMAGE:6971771 5', mRNA sequence.
ACCESSION CD559533
VERSION CD559533
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 492)
NIH-MGC http://nigc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585601.
Contact: Daniela S. Gerhardt, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@nci.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMU at:
http://image.llnl.gov

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High quality sequence stop: 492.  
Location/Qualifiers

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PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxp sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Karl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

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## ORIGIN

## Alignment Scores:

Pred. No.:	1.88e-44	Length:	492
Score:	430.00	Matches:	87
Percent Similarity:	77.61%	Conservative:	17
Best Local Similarity:	64.93%	Mismatches:	30
Query Match:	61.78%	Indels:	0
DB:	6	Gaps:	0

US-10-787-382-5 (1-134) x CD55953 (1-492)

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Qy 1 MetArgMetLeuLeuAanLeuSerLeuLeuAlaAlaTyValSerAlaPhe 20
    |||
Db 56 ATGAGAGATGCTTGCATTGAGTTGCTAGCTCTGAGCTGCTACGTATGCCATC 115
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Qy 21 AlavaGluAenPrometAanArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
    |||
Db 116 CCCACAGAAATCCACAGATGATGGTGAAGAAGCTTGACATGCTTCTTACTCAT 175
    |||
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAenLysAsnHis 60
    |||
Db 176 CGAAGCTGCTGATGAGCAATGAGACTCTGAGATTCCTGTTCTGTACATTAATAATCAC 235
    |||
Qy 61 GluLeuCyAlleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80
    |||
Db 236 CAAGCTGAGCTGAAGAAATCTTCAAGGAAATAGGCACACTGAGAGCAAACTGTGCAA 295
    |||
Qy 81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuLysGluHisIleGluArg 100
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Db 296 GGGGGTACTGTGAAAGACTATTCAAAATCTTCTTAATAAAGAAATACATGACGCC 355
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Qy 101 GlnLysLysArgCyAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
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Db 356 CAAATAAAGAGTGTGAGAGAAAGACGAGAGATTAACCAATTCCTAGACTACTGCAA 415
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Qy 121 ValPheLeuGlyValIleAenThrGluThrProGluSer 134
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Db 416 GAGTTCTGTGTATGAAACACGAGTGAATATAGAAAGT 457
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LOCUS Homo sapiens cDNA clone IMAGE:6971768, containing frame-shift
DEFINITION

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errors.  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 458)  
 Strauberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedlin, T.B., Toshitsuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smolins, D.E., Schermer, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 12477932  
 2 (bases 1 to 458)  
 Strauberg, R.  
 Direct Submission  
 Submitted (03-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabgs-remail.nih.gov](mailto:cgabgs-remail.nih.gov)  
 Tissue Procurement: Narayan Bhat  
 cDNA Library Preparation: Bhat Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www.shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcgdpaxil@stanford.edu](mailto:mcgdpaxil@stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R.M.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLT at: <http://image.llnl.gov>  
 Service: IRAX Plate: 172 Row: a Column: 15  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28555032  
 This clone has the following problem: frame shifted.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
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 /tissue\_type="PCR rescued clones"  
 /clone\_lib="NIH MGC\_195"  
 /lab\_host="DH10B"  
 /note="Vector: pDNR-Dual"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 7,86e-43 Length: 458  
 Score: 417.00 Matches: 87  
 Percent Similarity: 77.04% Conservative: 17

Best Local Similarity: 64.44% Mismatches: 30  
 Query Match: 59.91% Indels: 1  
 DB: 3 Gaps: 0  
 US-10-787-382-5 (1-134) x BC066279 (1-458)  
 Oy 1 MetArgMetLeuLeuAanLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20  
 24 ATGAGATGCTCTTCGATTCATTTAGTTCTGACCTTGGAGCTGCTGATGATGCCATC 83  
 Oy 21 AlAvalGlnaPnProMetAaMArgLeuValAlaGlnThrLeuThrLeuLeuSerThrHis 40  
 84 CCCACAGAAATTCACCAAGACGATGCTGGAAGACAGACCTGGACGACTTCTTACATCAT 143  
 Oy 41 ArgThrTrpLeuIleGlyArgGlyAsnLeuMetIleProThrProGlnAsnLeuAsnHis 60  
 144 CGAAGCTGCTGGAAGGCAATGACACTGTAGAGATTCCTGCTGATCAATAAATCAAC 203  
 Oy 61 GlnLeuCySileLeuGValPheGlnGlyIleLeuPThrLeuLysAsnGlnThrAlaHis 80  
 204 CAACTGCTGCTGCAAGAAATCTTTCAAGGANTAGGACACTGAGACTCAAACTGTGCA 263  
 Oy 81 GlyGlnAlaValAaPLeuLysLeuPheGlnAsnLeuSerLeuLeuGlyHisIleGlyArg 100  
 264 GGGGCTACTGCTGGAAGACATATTCAAAAATTGCTTAATTAAGAAATACATGACGCGC 323  
 Oy 101 Gln-LysLeuArgCysAlaGlyGlnArgTTPArgValThrLysPheLeuAaPlyrLeuG 120  
 324 CAAAAAAGGAGGTGAG 383  
 Oy 120 nvalPheLeuGlyValIleLeuThrGluTrpThrProGlnSer 134  
 Db 384 AGAGTTCTTGTTGATTAATGAACCGAGTGTGATTAATGAAGT 426  
 RESULT 7  
 BC066280  
 LOCUS Homo sapiens cDNA clone IMAGE:6971769, containing frame-shift errors.  
 DEFINITION BC066280 458 bp mRNA linear HTC 12-FEB-2004  
 ACCESSION BC066280.1 GI:42490838  
 VERSION BC066280.1  
 KEYWORDS HTC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 458)  
 Strauberg, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Klausner, R.D., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedlin, T.B., Toshitsuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smolins, D.E., Schermer, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 12477932  
 2 (bases 1 to 458)  
 Strauberg, R.  
 Direct Submission  
 Submitted (03-FEB-2004) National Institutes of Health, Mammalian

REMARK  
COMMENT

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project url: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: Narayan Bhat  
 cDNA Library Preparation: Bhat Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
 Series: IRAC Plate: 172 Row: a Column: 16  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28559032  
 This clone has the following problem: frame shifted.

## FEATURES

## SOURCE

location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /clone="IMAGE:6971769"  
 /tissue\_type="PCR rescued clones"  
 /clone\_lib="NIH MGC\_195"  
 /lab\_host="DH10B"  
 /note="Vector: pDNR-Dual"

## ORIGIN

## Alignment Scores:

Pred. No.: 7.86e-43 Length: 458  
 Score: 417.00 Matches: 87  
 Percent Similarity: 77.04% Conservative: 17  
 Best Local Similarity: 64.44% Mismatches: 30  
 Query Match: 59.91% Indels: 1  
 Gaps: 0

US-10-787-382-5 (1-134) x BC066280 (1-458)

Qy 1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTYrValSerAlaPhe 20  
 Db 24 ATGAGGATGCTTTCGACATTGAGTTGCTACTGCTGAGCTGCTGACGTATGACATC 83  
 Qy 21 AlAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40  
 Db 84 CCCACAGAAATTCGCCACAGATGACATTTGGTGAAGAGACCTTGACCTCTTCTACTCAT 143  
 Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsnHis 60  
 Db 144 GAAACTCTGCTGATAGCCATGATGACCTTGAGGATCTCTGTTCTCTGATCAATAAATCATC 203  
 Qy 61 GlnLeuCysIleLeuGluValPheGlnGlyIleAspThrLeuLeuYasnGlnThrAlaHis 80  
 Db 204 CAACGTGACACAGAAATCTTTCAGGGAATGAGCAACAGAGAGTCAAACTGTGCA 263  
 Qy 81 GlyIleValAlaValAspLeuPheGlnAsnLeuSerLeuIleGlyHisIleGluArg 100  
 Db 264 GGGGGTACTGTGGAAGAAGACTATTCAAAAATTGCTCTTAATAAGAAATACATGACGGC 323  
 Qy 101 Gln-LeuValAspCysAlaGlyGluArgTrpArgValThrLeuPheLeuAspTYrLeuG 120  
 Db 324 CAAAATAAAGATGTGAGAGAGAAAGACGAGAGATTAACCAATTCCTAGACTACGTGCA 383  
 Qy 120 nValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
 Db 384 AGAGTTCTTGCTGTATGAACACCGAGTGTGATATATAAAGT 426

RESULT 8

## CD559535

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

CD559535 463 bp mRNA linear EST 26-NOV-2003  
 AGENCOURT 14496865 NIH MGC\_195 Homo sapiens cDNA clone  
 IMAGE:6971769 5', mRNA sequence.  
 CD559535  
 CD559535.2 GI:38558950  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 463)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 On Jun 10, 2003 this sequence version replaced gi:31585603.  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: Narayan Bhat  
 cDNA Library Preparation: Bhat Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
 plate: IRBK1 row: 9 column: 08  
 High quality sequence stop: 463.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6971769"  
 /tissue\_type="mixed"  
 /lab\_host="DH5A (T1 phage-resistant)"  
 /clone\_lib="NIH MGC\_195"  
 /note="Vector: pDNR-Dual; Site 1: loxp-salt; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [ftp://image.lnl.gov/image/rearrayed\\_plates/IRBK-presv.dat](ftp://image.lnl.gov/image/rearrayed_plates/IRBK-presv.dat)  
 a Note: this is a NIH-MGC Library."

## FEATURES

## SOURCE

location/Qualifiers  
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 a Note: this is a NIH-MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 7.98e-43 Length: 463  
 Score: 417.00 Matches: 87  
 Percent Similarity: 77.04% Conservative: 17  
 Best Local Similarity: 64.44% Mismatches: 30  
 Query Match: 59.91% Indels: 1  
 Gaps: 0

US-10-787-382-5 (1-134) x CD559535 (1-463)

Qy 1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTYrValSerAlaPhe 20  
 Db 28 ATGAGGATGCTTTCGACATTGAGTTGCTACTGCTGAGCTGCTGACGTATGACATC 87  
 Qy 21 AlAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40

Db 88 CCCACAGAAATTCACAGATGCACTTGGTGAAGAGACTTGGCACTCTTCTACTCAT 147  
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60  
Db 148 CGAATCTGCTGATGAGCAATGAGACTCTGAGAGATTCCTGTCCTGTCATATAAATCAC 207  
Qy 61 GlnLeuCyb1LeuYsgLysValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80  
Db 208 CAACGTGCACTGAAGAAATCTTTCAGGAAATGAGCACATGAGAGTCAAACTGTGCA 267  
Qy 81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleYsgLysIleGluArg 100  
Db 268 GGGGGTACTGTGGAAGAAGCTATTCAAAACCTTCTTAATTAAGAAATACATGACGCC 327  
Qy 101 Gln-LysLysArgCysAlaGlyGluArgTTPArgValThrLysPheLeuAspTyrLeuG1 120  
Db 328 CAAAAAAGAAAAAGCTGAGAGAAAGACGAGAGTAACCAATTCCTAGACTACCTGCA 387  
Qy 120 nValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
Db 388 AGAGTTCTTGCTGTATGAAACCGAGTGAATATAGAAAGT 430

RESULT 9  
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ACCESSION CD559690  
VERSION CD559690.2 GI:38453490  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 467)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
On Jun 10, 2003 this sequence version replaced gi:31585758.  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: Bhat Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
Plate: IRBK1 row: 9 column: 07  
High quality sequence stop: 467.  
Location/Qualifiers  
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/note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:  
loxP-HindIII; Clones from this library have been  
PCR-amplified using gene-specific primers to contain the  
complete open reading frame (based on known gene sequences  
available from NCBI's RefSeq). Template for PCR is cDNA  
derived from either pooled cytoplasmic polyA RNA from 30  
cells lines or pooled total RNA from 10 different tissues  
(from BD Biosciences/Clontech and Washington University).  
PCR products are directionally cloned into the loxP sites  
of the pDNR-Dual vector. Library constructed by Dr.

ORIGIN  
Alignment Scores:  
Pred. No.: 8.07e-43 Length: 467  
Score: 417.00 Matches: 87  
Percent Similarity: 77.04% Conservative: 17  
Best Local Similarity: 64.44% Mismatches: 30  
Query Match: 59.91% Indels: 1  
DB: Gaps: 0  
US-10-787-382-5 (1-134) x CD559690 (1-467)

Qy 1 MetArgMetLeuAsnLeuSerLeuAlaLeuGlyAlaIleYrValSerAlaPhe 20  
Db 443 ATGAGAGATGCTTGTGCAATTTGAGTTGCTAGCTTGGAGCTGCTACGTATGCAATC 384  
Qy 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40  
Db 383 CCCACAGAAATTCACAGATGCACTTGGTGAAGAGACTTGGCACTCTTCTACTCAT 324  
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60  
Db 323 CGAATCTGCTGATGAGCAATGAGACTTGTGAGATTCCTGTCCTGTCATATAAATCAC 264  
Qy 61 GlnLeuCyb1LeuYsgLysValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80  
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Qy 81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleYsgLysIleGluArg 100  
Db 203 GGGGGTACTGTGGAAGAAGCTATTCAAAACCTTCTTAATTAAGAAATACATGACGCC 144  
Qy 101 Gln-LysLysArgCysAlaGlyGluArgTTPArgValThrLysPheLeuAspTyrLeuG1 120  
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Qy 120 nValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134  
Db 83 AGAGTTCTTGCTGTATGAAACCGAGTGAATATAGAAAGT 41

RESULT 10  
CD559689/c 473 bp mRNA linear EST 19-NOV-2003  
LOCUS AGENCOURT\_14496901 NIH\_MGC\_195 Homo sapiens cDNA clone  
DEFINITION IMAGE:6971769 5', mRNA sequence.  
ACCESSION CD559689  
VERSION CD559689.2 GI:38453487  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 473)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
On Jun 10, 2003 this sequence version replaced gi:31585757.  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: Bhat Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: <http://image.llnl.gov>

Plate: IRBK1 row: 9 column: 08  
High quality sequence start: 16  
High quality sequence stop: 473.  
Location/Qualifiers

## FEATURES

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/tissue\_type="mixed"  
/lab\_host="DH5A (T1 phage-resistant)"  
/clone\_1lb="NIH MGC 195"  
/note="Vector: pDNR-Dual; Site 1: loxp-Sali; Site\_2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [ftp://image.llnl.gov/image/rearrayed\\_plates/IRBK-presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBK-presv.dat)  
a Note: this is a NIH\_MGC library."

## ORIGIN

## Alignment Scores:

Pred. No.: 8.22e-43 Length: 473  
Score: 417.00 Matches: 87  
Percent Similarity: 77.04% Conservative: 17  
Best Local Similarity: 64.44% Mismatches: 30  
Query Match: 59.91% Indels: 1  
Gaps: 0

US-10-787-382-5 (1-134) x CD559689 (1-473)

1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20  
449 ATGAGGATGCTTGGCATTTGAGTTGCTAGCTCTGGAGCTGCTACGTATGATCCATC 390  
21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40  
389 CCCACAGAAATTCACCAAGATGCTGTAAGAGACCTTGCGCATGCTTCTTACTCAT 330  
41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsnHis 60  
329 CGAATCTGCTGATAGCCAAATGAGACTCTGAGATTCCTGTTCCGTACATATAAAATAC 270  
61 GlnLeuGlyIleLeuGluValPheGlnGlyIleAspThrLeuLeuAsnGlnThrAlaHis 80  
269 CAATCTGCACCTGAGAAATCTTTCAGGGAATGAGCACTGAGAGAGCAATCTGTCAA 210  
81 GlyGluAlaValAspPheLeuPheGlnAsnLeuSerLeuIleLeuGluHisIleGluArg 100  
209 GGGGGTACTGTGGAAGAAGACTAATCAAAAAGCTGCTTAATTAAGAAATACATGACGCG 150  
101 Gln-LysLeuArgCysAlaGlyGluArgTyrArgValThrLysPheLeuAspTyrLeuG 120  
149 CAAAAAAGAAAGTGTGAGAAAGAAAGACGAGAGATTAACCAATTCCTAGACTACTGCA 90  
120 nvalPheLeuGlyValIleAsnThrGluThrProGluSer 134  
89 AGAGTTCTTGCTGTATGACACCGAGTGTGATATAGAAACT 47

RESULT 11

## CD559536

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITL

## JOURNAL

## COMMENT

CD559536 489 bp mRNA linear EST 26-NOV-2003  
AGENCOURT 14496804 NIH MGC 195 Homo sapiens CDNA clone  
IMAGE:6971768 5', mRNA sequence.  
CD559536  
CD559536.2 GI:38558953  
EST.  
Homo sapiens (human)  
Homo sapiens  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 489)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
On Jun 10, 2003 this sequence version replaced gi:31585604.  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Narayan Bhat  
CDNA Library Preparation: Bhat Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: <http://image.llnl.gov>  
Plate: IRBK1 row: 9 column: 07  
High quality sequence start: 17  
High quality sequence stop: 489.  
Location/Qualifiers

## FEATURES

## source

1..489  
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/lab\_host="DH5A (T1 phage-resistant)"  
/clone\_1lb="NIH MGC 195"  
/note="Vector: pDNR-Dual; Site 1: loxp-Sali; Site\_2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [ftp://image.llnl.gov/image/rearrayed\\_plates/IRBK-presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBK-presv.dat)  
a Note: this is a NIH\_MGC library."

## ORIGIN

## Alignment Scores:

Pred. No.: 8.61e-43 Length: 489  
Score: 417.00 Matches: 87  
Percent Similarity: 77.04% Conservative: 17  
Best Local Similarity: 64.44% Mismatches: 30  
Query Match: 59.91% Indels: 1  
Gaps: 0

US-10-787-382-5 (1-134) x CD559536 (1-489)

1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20  
54 ATGAGGATGCTTGGCATTTGAGTTGCTAGCTCTGGAGCTGCTACGTATGATCCATC 113



TITLE	Perleira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.					
JOURNAL	Interfering nonneutral evolution from human-chimp-mouse orthologous gene clones					
PUBMED	Science 302 (5652), 1960-1963 (2003)					
REFERENCE	14671302					
AUTHORS	2 (bases 1 to 405)					
	Clark,A.G., Glanowski,S., Nelson,R., Thomas,P., Keiravai,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perleira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.					
	Direct Submission					
	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA					
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment:					
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	/db_xref="taxon:9598"					
gene	<1...>405					
	/gene="TL5"					
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Score:	411.00	Matches:	85			
Percent Similarity:	75.37%	Conservative:	16			
Best Local Similarity:	63.43%	Mismatches:	33			
Query Match:	59.05%	Gaps:	0			
DB:	9	Indels:	0			
US-10-787-382-5 (1-134) x AY412021 (1-405)						
CY	1	MetAAGMeLLeuLeuAsnLeuSerLeuLeuAlaLeuGlyValAlaTyrValSerAlaPhe	20			
Dd	1	ATGAAGATGCTTCGTGCATTGTAGTTGGCTTGACCTCTTGAGCGCTCAGCGTAGTACC	60			
CY	21	AlaValGluAsnProMetAsnArgLeuValAlaGlnThrLeuThrLeuLeuSerThrHis	40			
Dd	61	CCCAAGAAATCCCAACAAGTGCATTGGTGAAGAAGACTTGCGCATCTCTTA	120			
CY	41	ArghTrTPLeuIIGLyAspGlyAsnLeuNecIIeProThrProGluAsnLysAsnHis	60			
Dd	121	CGAACCTGCTAAATGCCAATAGACCTCGAGGATTCCTGTTCCGTGCATMAAATAC	180			
CY	61	GlnLeuCySiLeuGlyValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis	80			
Dd	181	CACCMNNGACGTGAAGAATCTTTTCAGGGAATAGGCACTCGAAGTCAAACCTGTGCA	240			
CY	81	GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIIGlyArg	100			
Dd	241	GGGGGTACTGTGGAAGAAGACTATCAAAAACCTGCTTAATAAATAATACATTANGGC	300			
CY	101	GlnLysLysArgCysAlaGlyGlnLysArgTPrpArgValIThrLysPheLeuAspTyrl	120			
Dd	301	CAAAAAAAAGATGTGGAGAAAGAAAGACCGAAGATGAACCAATTCCTAGACTTA	360			
CY	121	ValPheLeuGlyValIleAsnThrGlnTrpThrProGluSer	134			
Dd	361	GAGTTTCTTGTTGATATGAAACCGAAGTGGATTAATAGAAAGT	402			
RESULT 14						
LOCUS	BC066281					
DEFINITION	Homo sapiens cDNA clone IMAGE:6971770, containing frame-shift errors-					
VERSION	BC066281.1 GI:42490969					
KEYWORDS	HTC.					
SOURCE	Homo sapiens (human)					

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 456)
AUTHORS	Strauberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D., Altshuler,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhac,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scieczek,T.E., Brownstein,M.U., Uddin,T.B., Tonhyuk,I.S., Canninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McGowan,P.J., McGernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Woley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulk,S.W., Villalon,D.K., Muzny,D.M., Sodegren,E.J., Lu,X., Gibbs,R.A., Fahey,J.J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bonifard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E., Schmerch,A., Schein,J.E., Jones,S.J. and Marx,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932
TITLE	2 (bases 1 to 456)
JOURNAL	Strauberg,R.
PUBMED	Direct Submission
REFERENCE	Submitted (03-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
TITLE	NIH-MGC Project URL: http://mgc.nci.nih.gov
JOURNAL	Contact: MGC help desk
PUBMED	Email: gcgabs@mail.nih.gov
REFERENCE	Tissue Procurement: Narayan Bhat
TITLE	cDNA Library Preparation: Bhat Laboratory
JOURNAL	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
PUBMED	DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, CA 94305
REFERENCE	Web site: http://www.sbgc.stanford.edu
TITLE	Contact: (Dickson, Mark) mcd@xll.stanford.edu
JOURNAL	Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
PUBMED	R. M.
REFERENCE	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
TITLE	Series: IRAX Plate: 172 Row: a Column: 17
JOURNAL	This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 2855032
PUBMED	This clone has the following problem: frame shifted.
REFERENCE	Location/Qualifiers
TITLE	1..456
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REFERENCE	/db_xref="taxon:9606"
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JOURNAL	/cisseq_type="PCR rescued clones"
PUBMED	/clone_id="NIH_MGC_195"
REFERENCE	/lab_host="DH10B"
TITLE	/note="Vector: pDNR-Dual"
JOURNAL	ORIGIN
PUBMED	Alignment Scores:
REFERENCE	Pred. NO.:
TITLE	Score:
JOURNAL	Percent Similarity:
PUBMED	Best Local Similarity:
REFERENCE	Query Match:
TITLE	DB:
JOURNAL	Gaps:
PUBMED	Length:
REFERENCE	Matches:
TITLE	Conservative:
JOURNAL	Mismatch:
PUBMED	Indels:
REFERENCE	1
TITLE	0
JOURNAL	US-10-787-382-5 (1-134) x BC066281 (1-456)

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Db 84 CCCACAGAAATTCACAGAGCATTTGGTGAAGAAGACTTGCGACCTGCTTACTCAT 143
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
Db 144 CGAACTGCTGATGACCAATGAGACTCTGAGGATTCCTGTTCTGTACATAAATACAC 203
Qy 61 GlnLeuCySileLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80
Db 204 CACTGTGCACTGAGAAATCTTTGAGGAATAGGACACCTGGAGACCAATCTGTGCA 263
Qy 81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
Db 264 GGGGGTACTGTGGAAGAAGCTATTCAAAACTTGCTTAAATGAAGAAATACATTGA-CGG 322
Qy 101 GlnLysLysArgCySalaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
Db 323 CCAAAAAAAGTGTGAGAAAGAACGAGAGTAACCAATTCCTAGACTACCTGCA 382
Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
Db 383 GAGTTCTTGGTGAATGACACCGAGTGATTAATAGAAAGT 424

RESULT 15
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LOCUS AGNCOURT_14496964 NIH_MGC_195 Homo sapiens cDNA clone
DEFINITION IMGB:6971770 5', mRNA sequence.
ACCESSION CD559688
VERSION CD559688.2 GI:38453486
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 467)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585756.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgsdpb-remail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRBK1 row: 9 column: 09
High quality sequence start: 11
High quality sequence stop: 467.
Location/Qualifiers
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/lab_host="DH5A (TI phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual1, Site 1: loxP-Sali; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the

```

complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [http://image.llnl.gov/image/rearayed\\_plates/IRBK.presv.dat](http://image.llnl.gov/image/rearayed_plates/IRBK.presv.dat)  
a Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.:	2,07e-41	Length:	467
Score:	406.00	Matches:	87
Percent Similarity:	76.87%	Conservative:	16
Best Local Similarity:	64.93%	Mismatches:	31
Query Match:	58.33%	Indels:	1
DB:	6	Gaps:	0

US-10-787-382-5 (1-134) x CD559688 (1-467)

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Qy 1 MetArgMetLeuLeuAnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20
Db 443 ATGAGAGATGCTTGGCATTTGAGTTGCTAGCTTGAGAGCTGCTAGCTAGTAAATCCATC 384
Qy 21 AlAlaValGluAenPrometAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40
Db 383 CCCACAGAAATTCACAGAGCATTTGGTGAAGAAGACTTGCGACCTGCTTACTCAT 324
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
Db 323 CGAACTGCTGATGACCAATGAGACTCTGAGGATTCCTGTTCTGTACATAAATACAC 264
Qy 61 GlnLeuCySileLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80
Db 263 CACTGTGCACTGAGAAATCTTTGAGGAATAGGACACCTGGAGACCAATCTGTGCA 204
Qy 81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
Db 203 GGGGGTACTGTGGAAGAAGCTATTCAAAACTTGCTTAAATGAAGAAATACATTGA-CGG 145
Qy 101 GlnLysLysArgCySalaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
Db 144 CCAAAAAAAGTGTGAGAAAGAACGAGAGTAACCAATTCCTAGACTACCTGCA 85
Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
Db 84 GAGTTCTTGGTGAATGACACCGAGTGATTAATAGAAAGT 43

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Search completed: August 7, 2005, 00:10:27  
Job time : 2821 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 6, 2005, 19:38:05 ; Search time 2111.1 Seconds  
(without alignments)  
2639.542 Million cell updates/sec

Title: US-10-787-382-10  
 Perfect score: 610  
 Sequence: 1 FAVENPMNRLVAETTLTST.....FLDYLGQVPGVINTWTPES 115

Scoring table:		BLOSUM62
Xgapop	10.0	Xgapext 0.5
Ygapop	10.0	Ygapext 0.5
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Delop	6.0	Delext 7.0

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Searched:      470823 segs, 24227607955 residues
Total number of hits satisfying chosen parameters:  9416466
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Command line parameters:
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-DB=gemblib -GPRM=faastap -SUFFIX=rge -MINMATCH=0.1 -LOOPT=0 -LOPEXT=45
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DLOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGESUBRAY -NEG SCORES=0 -WAIT -DSBLCAT=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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GenEmbL:.*
1: gb_da.*
2: gb_htg.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
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10: gb_ro.*
11: gb_atg.*
12: gb_ey.*
13: gb_un.*
14: gb_vi.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	610	100.0	345	6	BD211562	BD211562 Canine a
C 2	610	100.0	345	6	BD211563	BD211563 Canine a
C 3	610	100.0	345	6	AR241540	AR241540 Sequence
C 4	610	100.0	345	6	AR241541	AR241541 Sequence

5	610	100.0	345	AR254496	AR254496 Sequence
c	6	610	100.0	AR254497	AR254497 Sequence
7	610	100.0	402	BD211560	BD211560 Canine an
c	8	610	100.0	BD211561	BD211561 Canine an
9	610	100.0	402	AR241538	AR241538 Sequence
c	10	610	100.0	AR241539	AR241539 Sequence
11	610	100.0	402	AR254494	AR254494 Sequence
c	12	610	100.0	AR254495	AR254495 Sequence
13	610	100.0	402	AR331919	AR331919 Canis fam
c	14	610	100.0	BD211558	BD211558 Canine an
15	610	100.0	610	BD211559	BD211559 Canine an
c	16	610	100.0	AR241536	AR241536 Sequence
17	610	100.0	610	AR241537	AR241537 Sequence
c	18	610	100.0	AR254492	AR254492 Sequence
19	610	100.0	610	AR254493	AR254493 Sequence
c	20	601	98.5	AR300436	AR300436 Sequence
21	601	98.5	405	AX083939	AX083939 Sequence
22	563	92.3	356	AF091133	AF091133 Canis fam
23	510	83.6	838	AF025436	AF025436 Felis cat
24	505	82.8	405	AF068770	AF068770 Felis cat
25	501	82.1	405	SSC010088	SSC010088 Sus scrofa
26	501	82.1	529	SSC133452	SSC133452 Sus scrofa
27	494	81.0	405	ECU91947	ECU91947 Equus caball
28	491	80.5	405	BTINTLE05	BTINTLE05 B. taurus mr
29	487	79.8	520	OAUS3038	OAUS3038 Ovis aries
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31	439	72.0	354	AP051372	AP051372 Felis cat
32	382	62.6	405	AF294756	AF294756 Salintri B
33	372	61.0	564	CPU34588	CPU34588 Cavia porce
34	362.5	59.4	1658	AF331920	AF331920 Canis fam
c	35	361	59.2	6 A00350	A00350 Artificial
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37	361	59.2	405	9 CEYIN5A	126033 Carcobeus
38	358	58.7	628	10 MERIT1A	137780 Meriones un
39	357	58.5	864	6 AX766525	AX766525 Sequence
40	356	58.4	421	12 SYNT15A	M33949 Synthetic h
41	356	58.4	459	9 BC066282	BC066282 Homo sapi
42	356	58.4	816	6 CO721603	CO721603 Sequence
43	356	58.4	816	6 E01639	E01639 cDNA encodi
44	356	58.4	816	6 E13591	E13591 cDNA encodi
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## ALIGNMENTS

RESULT 1	LOCUS	DEFINITION
BD211562	345 bp	DNA linear PAT 17-JUL-2003
		Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same.

REFERENCE AUTHORS TITLE JOURNAL	COMMENT
1 (bases 1 to 345) Shi,G., Yang,S., Dreitz,M.J. and Wonderling,R.S. Canine and feline immunoregulatory proteins, nucleic acid molecules Patent: JP 2002516104-A 68 04-JUN-2002; HESKA CORP	Canis familiaris (dog)

PF 28-MAY-1999 JP 20000551002  
PR 29-MAY-1998 US 60/087306  
PI GEORGE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC  
C12A15/09, A61K31/7088, A61K38/00, A61K38/21, A61K39/00, A61K39/3935,  
PC A61K39/3935  
PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,  
PC C07K14/54,

PC C07K14/56, C07K14/705, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC  
G01N33/15,  
PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine  
and feline immunoregulatory proteins, nucleic acid CC  
molecules and  
CC method of using the same  
FT Key Location/Qualifiers  
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ORIGIN

Alignment Scores:

Pred. No.:	8 386-67	Length:	345
Score:	610.00	Matches:	115
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-787-382-10 (1-115) x BD211562 (1-345)

QY 1 PheAlaValGluAnPromeTAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20  
1 TTTGCTGTAGAAAATCCCATGATAGACTGTGTGCAGAGACTTGACACCTGCTCCACT 60  
DB 1 TTTGCTGTAGAAAATCCCATGATAGACTGTGTGCAGAGACTTGACACCTGCTCCACT 60

QY 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40  
61 CATGAACCTGGCTGATAGAGGAGATGGAACTGATGATCTTCTCTGAAAAATAAAAAT 120  
DB 61 CATGAACCTGGCTGATAGAGGAGATGGAACTGATGATCTTCTCTGAAAAATAAAAAT 120

QY 41 HisGlnLeuCysIleLeuGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
121 CACCACTGTGCTATTAAGAGATTTCAGGGATATAGACATTTGAAGAACCAACTGCC 180  
DB 121 CACCACTGTGCTATTAAGAGATTTCAGGGATATAGACATTTGAAGAACCAACTGCC 180

QY 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80  
181 CACGGGAGGCTGTGATTAACCTATTCCTTCTTAAATTAAGAACCATAGAG 240  
DB 181 CACGGGAGGCTGTGATTAACCTATTCCTTCTTAAATTAAGAACCATAGAG 240

QY 81 ArgGlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100  
241 CGCCAAAAAAGAGGTGTGAGAGAAAGATGAGAGATGACAAAGTTCTTAGACTACTG 300  
DB 241 CGCCAAAAAAGAGGTGTGAGAGAAAGATGAGAGATGACAAAGTTCTTAGACTACTG 300

QY 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
301 CAAGTATTTCTTGTTGATTAACACGAGTGGACCGGAAAGT 345  
DB 301 CAAGTATTTCTTGTTGATTAACACGAGTGGACCGGAAAGT 345

RESULT 2  
BD211563 345 bp DNA linear PAT 17-JUN-2003  
LOCUS Canine and feline immunoregulatory proteins, nucleic acid molecules  
DEFINITION and method of using the same.  
ACCESSION BD211563  
VERSION BD211563.1 GI:33021333  
KEYWORDS JP 2002516104-A/69.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 345)  
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules  
and method of using the same  
JOURNAL Patent: JP 2002516104-A 69 04-JUN-2002;  
HESKA CORP  
OS Canis familiaris (dog)  
PN JP 2002516104-A/69  
PD 04-JUN-2002  
PR 28-MAY-1999 JP 2000551002  
PI 29-MAY-1998 US 60/087306  
GKKEE SIM,SHOJIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC

C12N15/09, A61K31/7088, A61K38/00, A61K38/21, A61K39/00, A61K39/395,  
PC A61K39/395,  
PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,  
PC C07K14/54,  
PC C07K14/56, C07K14/705, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC  
G01N33/15,  
PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine  
and feline immunoregulatory proteins, nucleic acid CC  
molecules and  
CC method of using the same  
FT Key Location/Qualifiers  
CDS 1..345  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9615"

ORIGIN

Alignment Scores:

Pred. No.:	8 386-67	Length:	345
Score:	610.00	Matches:	115
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-787-382-10 (1-115) x BD211563 (1-345)

QY 1 PheAlaValGluAnPromeTAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20  
345 TTTGCTGTAGAAAATCCCATGATAGACTGTGTGCAGAGACTTGACACCTGCTCCACT 286  
DB 345 TTTGCTGTAGAAAATCCCATGATAGACTGTGTGCAGAGACTTGACACCTGCTCCACT 286

QY 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40  
285 CATGAACCTGGCTGATAGAGGAGATGGAACTGATGATCTTCTCTGAAAAATAAAAAT 226  
DB 285 CATGAACCTGGCTGATAGAGGAGATGGAACTGATGATCTTCTCTGAAAAATAAAAAT 226

QY 41 HisGlnLeuCysIleLeuGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
225 CACCACTGTGCTATTAAGAGATTTCAGGGATATAGACATTTGAAGAACCAACTGCC 166  
DB 225 CACCACTGTGCTATTAAGAGATTTCAGGGATATAGACATTTGAAGAACCAACTGCC 166

QY 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80  
165 CACGGGAGGCTGTGATTAACCTATTCCTTCTTAAATTAAGAACCATAGAG 106  
DB 165 CACGGGAGGCTGTGATTAACCTATTCCTTCTTAAATTAAGAACCATAGAG 106

QY 81 ArgGlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100  
105 CGCCAAAAAAGAGGTGTGAGAGAAAGATGAGAGATGACAAAGTTCTTAGACTACTG 46  
DB 105 CGCCAAAAAAGAGGTGTGAGAGAAAGATGAGAGATGACAAAGTTCTTAGACTACTG 46

QY 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
45 CAAGTATTTCTTGTTGATTAACACGAGTGGACCGGAAAGT 1  
DB 45 CAAGTATTTCTTGTTGATTAACACGAGTGGACCGGAAAGT 1

RESULT 3  
AR241540 345 bp DNA linear PAT 20-DEC-2002  
LOCUS Sequence 85 from patent US 6471957.  
DEFINITION AR241540  
ACCESSION AR241540  
VERSION AR241540.1 GI:27287249  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 345)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-4 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6471957-A 85 29-OCT-2002;  
FEATURES Location/Qualifiers  
1..345  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

## Alignment Scores:

Pred. No.: 8.38e-67 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-787-382-10 (1-115) x AR241540 (1-345)

Qy 1 PheAlaValaGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 1 TTGGCTGTAGAAATCCCATGAAATAGACTGTGGCAAGACCTTGACACTGCTCCACT 60  
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsn 40  
Db 61 CATCGAATTGGCTGTAGATGGAGTGGAACTGATGATTCCTTACTCTGAAAAATAAAAAT 120  
Qy 41 HisGlnLeuCySrlleYsgIuValPheGlnGlyIleAspThrLeuYsaAngIntThra 60  
Db 121 CACCACTGTGCACTTAAAGAAAGTTTTCAGGGTATAGACATGAAAGAACCAAACTGCC 180  
Qy 61 HisGlyIuValaValaAspIleYsaLeuPheGlnAsnLeuSerLeuIleYsgIuHisIleGlu 80  
Db 181 CACGGGAGGCTGTGATTAACCTATTCCTTAATTAAGAACACATAGAG 240  
Qy 81 ArgGlnIleYsaArgCySalaGlyIuArgTrpArgValThrIlyspPheLeuAspTrpLeu 100  
Db 241 CGCCAAAAAAGGTGTGACGAGGAAGATGAGAGTGAACAAAGTTCCTAGACTACTG 300  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 301 CAAGTATTTCTGTGTATTAACACCGAGTGCACCGGAAAGT 345

## RESULT 4

AR241541/c AR241541 345 bp DNA linear PAT 20-DEC-2002  
LOCUS Sequence 87 from patent US 6471957.

DEFINITION AR241541  
ACCESSION AR241541 GI:27287250  
VERSION AR241541.1 GI:27287250  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 345)  
AUTHORS Sim,G.-K., Yang,S., Drelitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-4 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6471957-A 87 29-OCT-2002;

FEATURES  
Source Location/Qualifiers  
1..345  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

## Alignment Scores:

Pred. No.: 8.38e-67 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-787-382-10 (1-115) x AR241541 (1-345)

Qy 1 PheAlaValaGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 345 TTGGCTGTAGAAATCCCATGAAATAGACTGTGGCAAGACCTTGACACTGCTCCACT 286  
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsn 40  
Db 285 CATCGAATTGGCTGTAGATGGAGTGGAACTGATGATTCCTTACTCTGAAAAATAAAAAT 226

Qy 41 HisGlnLeuCySrlleYsgIuValPheGlnGlyIleAspThrLeuYsaAngIntThra 60  
Db 225 CACCACTGTGCACTTAAAGAAAGTTTTCAGGGTATAGACATGAAAGAACCAAACTGCC 166

Qy 61 HisGlyIuValaValaAspIleYsaLeuPheGlnAsnLeuSerLeuIleYsgIuHisIleGlu 80  
Db 165 CACGGGAGGCTGTGATTAACCTATTCCTGCTTAATTAAGAACACATAGAG 106

Qy 81 ArgGlnIleYsaArgCySalaGlyIuArgTrpArgValThrIlyspPheLeuAspTrpLeu 100  
Db 105 CGCCAAAAAAGGTGTGACGAGGAAGATGAGAGTGAACAAAGTTCCTAGACTACTG 46

Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 45 CAAGTATTTCTGTGTATTAACACCGAGTGCACCGGAAAGT 1

## RESULT 5

AR254496 AR254496 345 bp DNA linear PAT 20-DEC-2002  
LOCUS Sequence 85 from patent US 6482403.

DEFINITION AR254496  
ACCESSION AR254496  
VERSION AR254496.1 GI:27303384  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 345)  
AUTHORS Sim,G.-K., Yang,S., Drelitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-13 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6482403-A 85 19-NOV-2002;

FEATURES  
Source Location/Qualifiers  
1..345  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

## Alignment Scores:

Pred. No.: 8.38e-67 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-787-382-10 (1-115) x AR254496 (1-345)

Qy 1 PheAlaValaGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 1 TTGGCTGTAGAAATCCCATGAAATAGACTGTGGCAAGACCTTGACACTGCTCCACT 60  
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsn 40  
Db 61 CATCGAATTGGCTGTAGATGGAGTGGAACTGATGATTCCTTACTCTGAAAAATAAAAAT 120  
Qy 41 HisGlnLeuCySrlleYsgIuValPheGlnGlyIleAspThrLeuYsaAngIntThra 60  
Db 121 CACCACTGTGCACTTAAAGAAAGTTTTCAGGGTATAGACATGAAAGAACCAAACTGCC 180  
Qy 61 HisGlyIuValaValaAspIleYsaLeuPheGlnAsnLeuSerLeuIleYsgIuHisIleGlu 80  
Db 181 CACGGGAGGCTGTGATTAACCTATTCCTGCTTAATTAAGAACACATAGAG 240  
Qy 81 ArgGlnIleYsaArgCySalaGlyIuArgTrpArgValThrIlyspPheLeuAspTrpLeu 100  
Db 241 CGCCAAAAAAGGTGTGACGAGGAAGATGAGAGTGAACAAAGTTCCTAGACTACTG 300  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 301 CAAGTATTTCTGTGTATTAACACCGAGTGCACCGGAAAGT 345

## RESULT 6

AR254497/c AR254497 345 bp DNA linear PAT 20-DEC-2002  
LOCUS

DEFINITION Sequence 87 from patent US 6482403.  
ACCESSION AR254497  
VERSION AR254497.1 GI:27303385  
SOURCE  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 345)  
AUTHORS Sim,G.-K., Yang,S., Drelitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-13 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6482403-A 87 19-NOV-2002;  
FEATURES  
source Location/Qualifiers  
1..345  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 8,38e-67 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-787-382-10 (1-115) x AR254497 (1-345)

QY 1 PheAlaValAGluAenPromeTAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20  
Db TTTCGTGTAGAAATCCCATGATAGACTGTGTGCAAGACTTGACACTGCTCCACT 266

QY 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40  
Db CATGAACCTGGCGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAT 226

QY 41 HisGlnLeuCyseIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
Db CACCACTGTGCATTAAAGAAAGTTTTCAGGGATATGACACATTGAAGAACCAAACTGCC 166

QY 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80  
Db CACGGGAGGCTGTGATTAACCTATTCAAAACCTGCTTTAATAAAGAACACATAGAG 106

QY 81 ArgGlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100  
Db CGCCAAAAGAAAAAGGTGTGCGAGAAAGATGAGAGTGAACAAAGTCTTGAAGTACTG 46

QY 101 GlnValPheLeuGlyValIleAsnThrGluThrProGluSer 115  
Db 45 CAAGTATTTCTGTGTATTAACACCGAGTGAACCGGAAAGT 1

RESULT 7  
BD211560 402 bp DNA linear PAT 17-JUN-2003  
LOCUS Canine and feline immunoregulatory proteins, nucleic acid molecules  
DEFINITION and method of using the same.  
ACCESSION BD211560  
VERSION BD211560.1 GI:33021330  
KEYWORDS JP 2002516104-A/66.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE Sim,G., Yang,S., Drelitz,M.J. and Wonderling,R.S.  
AUTHORS Canine and feline immunoregulatory proteins, nucleic acid molecules  
TITLE and method of using the same  
JOURNAL Patent: JP 2002516104-A 66 04-JUN-2002;  
HESKA CORP  
OS Canis familiaris (dog)  
PN JP 2002516104-A/66  
PD 04-JUN-2002  
PF 28-MAY-1999 JP 2000551002

PR 29-MAY-1998 US 60/087306  
PI GERKER SIM,SHUMIN YANG,MATTHEW J DREITZ,RANANI S WONDERLING PC  
C12N15/00,A61K31/7088,A61K38/21,A61K39/00,A61K39/395,  
PC A61K39/395,  
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,  
PC C07K14/54,  
PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10,PC  
G01N33/15,  
PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine  
and feline immunoregulatory proteins, nucleic acid CC  
molecules and  
CC method of using the same  
FT Key Location/Qualifiers  
FT source 1..402  
/organism="Canis familiaris (dog)".  
/db\_xref="taxon:9615"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.01e-66 Length: 402  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-787-382-10 (1-115) x BD211560 (1-402)

QY 1 PheAlaValAGluAenPromeTAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20  
Db TTTCGTGTAGAAATCCCATGATAGACTGTGTGCAAGACTTGACACTGCTCCACT 117

QY 58 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40  
Db CATGAACCTGGCGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAT 177

QY 118 HisGlnLeuCyseIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
Db CACCACTGTGCATTAAAGAAAGTTTTCAGGGATATGACACATTGAAGAACCAAACTGCC 237

QY 178 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80  
Db CACGGGAGGCTGTGATTAACCTATTCAAAACCTGCTTTAATAAAGAACACATAGAG 297

QY 61 ArgGlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100  
Db 238 CGCCAAAAGAAAAAGGTGTGCGAGAAAGATGAGAGTGAACAAAGTCTTGAAGTACTG 357

QY 81 ArgGlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100  
Db 298 CGCCAAAAGAAAAAGGTGTGCGAGAAAGATGAGAGTGAACAAAGTCTTGAAGTACTG 357

QY 101 GlnValPheLeuGlyValIleAsnThrGluThrProGluSer 115  
Db 358 CAAGTATTTCTGTGTATTAACACCGAGTGAACCGGAAAGT 402

RESULT 8  
BD211561 402 bp DNA linear PAT 17-JUN-2003  
LOCUS Canine and feline immunoregulatory proteins, nucleic acid molecules  
DEFINITION and method of using the same.  
ACCESSION BD211561  
VERSION BD211561.1 GI:33021331  
KEYWORDS JP 2002516104-A/67.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE Sim,G., Yang,S., Drelitz,M.J. and Wonderling,R.S.  
AUTHORS Canine and feline immunoregulatory proteins, nucleic acid molecules  
TITLE and method of using the same  
JOURNAL Patent: JP 2002516104-A 67 04-JUN-2002;

COMMENT HESKA CORP  
OS Canis familiaris (dog)  
PN JP 2002516104-A/67  
PD 04-JUN-2002  
PF 28-MAY-1999 JP 2000551002  
PI 29-MAY-1998 US 60/087306  
PI GERKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC  
C12N15/09,A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,  
PC A61K39/395  
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,  
PC C07K14/54,  
PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC  
G01N33/15,  
PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine  
and feline immunoregulatory proteins, nucleic acid CC  
molecules and  
CC method of using the same  
FH Key Location/Qualifiers  
FT source 1..402  
FT /organism="Canis familiaris (dog)"  
FT Location/Qualifiers  
1..402  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9615"

ORIGIN  
Alignment Scores:  
Pred. No.: 1,01e-66 Length: 402  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 6

US-10-787-382-10 (1-115) x BD211561 (1-402)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20  
Db 345 TTGCTGTAGAAATCCCATGAATAGACTGTGGCAGAGACTTGACACTGCTCTCCACT 286

Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleAsn 40  
Db 285 CATGAACCTTGCTGATAGCGGATGGAACCTGATGATCTTCTCTGAAAAATAAAAAT 226

Qy 41 HisGlnLeuCyrllelysgValAlaPheGlnGlyIleAspThrLeuIleAsnGlnThrAla 60  
Db 225 CACCAACTGTGCAATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAACGACC 166

Qy 61 HisGlyValAlaValAlaAspIleAsnLeuPheGlnAsnLeuSerLeuIlelysgIleIleGlu 80  
Db 165 CACGGGAGAGCTGTGATTAACCTATTCCTTTAAATTAAGAACACATAGAG 106

Qy 81 ArgGlnIlelysgValAlaGlyIleAspThrTrpArgValThrIlePheLeuAspTrpLeu 100  
Db 105 CGCGAAAAAAGAGTGTGCGAGGAAAGATGAGAGTGAACAAAGTTCTTGACTTACTG 46

Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 45 CAAGTATTTCTTGCTGATTAACACCGAGTGACACCGAGAAAGT 1

RESULT 9  
LOCUS AR241538 402 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 83 from patent US 6471957.  
ACCESSION AR241538  
VERSION AR241538.1 GI:27287247  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 402)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.

TITLE Canine IL-4 Immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6471957-A 83 29-OCT-2002;  
FEATURES Location/Qualifiers  
SOURCE 1..402  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 1,01e-66 Length: 402  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 6

US-10-787-382-10 (1-115) x AR241538 (1-402)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20  
Db 58 TTGCTGTAGAAATCCCATGAATAGACTGTGGCAGAGACTTGACACTGCTCTCCACT 117

Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleAsn 40  
Db 118 CATGAACCTTGCTGATAGCGGATGGAACCTGATGATCTTCTCTGAAAAATAAAAAT 177

Qy 41 HisGlnLeuCyrllelysgValAlaPheGlnGlyIleAspThrLeuIleAsnGlnThrAla 60  
Db 178 CACCAACTGTGCAATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAACGACC 237

Qy 61 HisGlyValAlaValAlaAspIleAsnLeuPheGlnAsnLeuSerLeuIlelysgIleIleGlu 80  
Db 238 CACGGGAGAGCTGTGATTAACCTATTCCTTTAAATTAAGAACACATAGAG 297

Qy 81 ArgGlnIlelysgValAlaGlyIleAspThrTrpArgValThrIlePheLeuAspTrpLeu 100  
Db 298 CGCGAAAAAAGAGTGTGCGAGGAAAGATGAGAGTGAACAAAGTTCTTGACTTACTG 357

Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 358 CAAGTATTTCTTGCTGATTAACACCGAGTGACACCGAGAAAGT 402

RESULT 10  
LOCUS AR241539 402 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 84 from patent US 6471957.  
ACCESSION AR241539  
VERSION AR241539.1 GI:27287248  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 402)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-4 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6471957-A 84 29-OCT-2002;  
FEATURES Location/Qualifiers  
SOURCE 1..402  
/organism="unknown"  
/mol\_type="genomic DNA"

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Alignment Scores:  
Pred. No.: 1,01e-66 Length: 402  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 6

US-10-787-382-10 (1-115) x AR241539 (1-402)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20

Db 345 TTGCTGTAGAAAATCCCATGAATAGACTGTGTGCAAGACCTTGACACTGCTCTCCACT 286  
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsn 40  
Db 285 CATGAACCTTGCTGATAGCGATGGCACTGATGATTCCTTACTCTGAAAAATATAAAT 226  
Qy 41 HisGlnLeuCySilelysgluValPheGlnGlyIleAspThrLeuIleAsnGlnThrAla 60  
Db 225 CACCAACTGTGCATTAAGAAGTTTTCAGGGGTATAGACATTTGAAGAACCACCACTGCC 166  
Qy 61 HisGlyGluAlaValAspIleuPheGlnAsnLeuSerLeuIlelysgluHisIleGlu 80  
Db 165 CACGGGAGGCTGTGATTAACCTATCCAAACTGTCTTAATTAAGAACAACATAGAG 106  
Qy 81 ArgGlnIlyysArgCySalaGlyGluArgTrpArgValThrIlyspPheLeuAspTYrLeu 100  
Db 105 CGCCAAAAAAAAGAGTGTGCAGAGAAAGATGAGAGATGACAAAGTTCTTGACTACTG 46  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 45 CAAGTATTCTTGTGTATATTAACACCGAGTGACACCGGAAAGT 1

RESULT 11  
AR254494 402 bp DNA linear PAT 20-DEC-2002  
LOCUS AR254494 Sequence 83 from patent US 6482403.  
DEFINITION AR254494  
ACCESSION AR254494  
VERSION AR254494.1 GI:27303382  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 402)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-13 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6482403-A 83 19-NOV-2002;  
FEATURES  
source 1..402  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 1,01e-66 Length: 402  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 58 TTTCCTGTAGAAAATCCCATGAATAGACTGTGTGCAAGACCTTGACACTGCTCTCCACT 117  
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsn 40  
Db 118 CATGAACCTTGCTGATAGCGATGGCACTGATGATTCCTTACTCTGAAAAATATAAAT 177  
Qy 41 HisGlnLeuCySilelysgluValPheGlnGlyIleAspThrLeuIleAsnGlnThrAla 60  
Db 178 CACCAACTGTGCATTAAGAAGTTTTCAGGGGTATAGACATTTGAAGAACCACCACTGCC 237  
Qy 61 HisGlyGluAlaValAspIleuPheGlnAsnLeuSerLeuIlelysgluHisIleGlu 80  
Db 238 CACGGGAGGCTGTGATTAACCTATCCAAACTGTCTTAATTAAGAACAACATAGAG 297  
Qy 81 ArgGlnIlyysArgCySalaGlyGluArgTrpArgValThrIlyspPheLeuAspTYrLeu 100  
Db 298 CGCCAAAAAAAAGAGTGTGCAGAGAAAGATGAGAGATGACAAAGTTCTTGACTACTG 357

Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 358 CAAGTATTCTTGTGTATATTAACACCGAGTGACACCGGAAAGT 402  
RESULT 12  
AR254495/c 402 bp DNA linear PAT 20-DEC-2002  
LOCUS AR254495 Sequence 84 from patent US 6482403.  
DEFINITION AR254495  
ACCESSION AR254495  
VERSION AR254495.1 GI:27303383  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 402)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-13 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6482403-A 84 19-NOV-2002;  
FEATURES  
source 1..402  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 1,01e-66 Length: 402  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
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US-10-787-382-10 (1-115) x AR254495 (1-402)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
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Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsn 40  
Db 285 CATGAACCTTGCTGATAGCGATGGCACTGATGATTCCTTACTCTGAAAAATATAAAT 226  
Qy 41 HisGlnLeuCySilelysgluValPheGlnGlyIleAspThrLeuIleAsnGlnThrAla 60  
Db 225 CACCAACTGTGCATTAAGAAGTTTTCAGGGGTATAGACATTTGAAGAACCACCACTGCC 166  
Qy 61 HisGlyGluAlaValAspIleuPheGlnAsnLeuSerLeuIlelysgluHisIleGlu 80  
Db 165 CACGGGAGGCTGTGATTAACCTATCCAAACTGTCTTAATTAAGAACAACATAGAG 106  
Qy 81 ArgGlnIlyysArgCySalaGlyGluArgTrpArgValThrIlyspPheLeuAspTYrLeu 100  
Db 105 CGCCAAAAAAAAGAGTGTGCAGAGAAAGATGAGAGATGACAAAGTTCTTGACTACTG 46  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 45 CAAGTATTCTTGTGTATATTAACACCGAGTGACACCGGAAAGT 1

RESULT 13  
AF331919 610 bp mRNA linear MAM 04-OCT-2001  
LOCUS AF331919 Canis familiaris interleukin-5 mRNA, complete cds.  
DEFINITION AF331919  
ACCESSION AF331919  
VERSION AF331919.1 GI:15919180  
KEYWORDS  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 610)  
AUTHORS Yang,S., Sellins,K.S., Weber,E. and McCall,C.  
TITLE Canine interleukin-5: molecular characterization of the gene and expression of biologically active recombinant protein

JOURNAL J. Interferon Cytokine Res. 21 (6), 361-367 (2001)  
MEDLINE 21334408  
PUBMED 11440633  
REFERENCE 2 (bases 1 to 610)  
AUTHORS Yang, S.  
TITLE Direct Submission  
JOURNAL Submitted (22-DEC-2000) Immunology, Heeska Corporation, 1613  
Prospect Parkway, Ft Collins, CO 80525, USA  
FEATURES  
source location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
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29. .433  
/note="IL-5"  
/codon\_start=1  
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Pred. No.: 1.66e-66 Length: 610  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
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Qy 1 PheAlaValAlaGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20  
Db 86 TTTCCTGTAGAAAATCCCATATATGACTGTGGCAGAGACCTTGACACTCTCTCCACT 145  
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40  
Db 146 CATGAACTGGCTGATAGGCGATGGGAACTGATGATTCCTACTCTGAAAATRAAAAT 205  
Qy 41 HisGlnLeuCySileuVgIuValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
Db 206 CACCAACTGGCATTAAGAAGTTTTCAGGGTATGACACATTAAGAAGCAAACTGCC 265  
Qy 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80  
Db 266 CACGGGAGGCTGGATTAACATATTCCTCAAACTTGTCTTTAATTAAGAAGCAATAGAG 325  
Qy 81 ArgGlnLysLysArgCySAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100  
Db 326 CGCCAAAAGAGCTGGATTAACATATTCCTCAAACTTGTCTTTAATTAAGAAGCAATAGAG 385  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 386 CAAATATTTCTTGGTGTATTAACACCGAGTGAACCGGAAAGT 430  
RESULT 14  
BD211558 610 bp DNA linear PAT 17-JUN-2003  
LOCUS Canine and feline immunoregulatory proteins, nucleic acid molecules  
DEFINITION and method of using the same.  
ACCESSION BD211558  
VERSION BD211558.1 GI:33021328  
KEYWORDS JP 2002516104-A/64.  
SOURCE Canis familiaris (dog)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Plissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 610)

AUTHORS Sim, G., Yang, S., Dreitz, M.J. and Wonderling, R.S.  
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules  
JOURNAL Patent: JP 2002516104-A 64 04-JUN-2002;  
COMMENT HESKA CORP  
OS Canis familiaris (dog)  
PN 04-JUN-2002  
PD 04-JUN-2002  
PP 28-MAY-1998 JP 2000551002  
PR 29-MAY-1998 US 60/087306  
PI GEXKEB SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC  
C12N15/09, A61K31/7088, A61K38/00, A61K38/21, A61K39/00, A61K39/395,  
PC A61K39/395,  
PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,  
PC C07K14/54,  
PC C07K14/56, C07K14/705, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC  
G01N33/15,  
PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine  
and feline immunoregulatory proteins, nucleic acid CC  
molecules and  
CC method of using the same  
FT key location/Qualifiers  
FT CDS (29). (430).  
FEATURES  
source location/Qualifiers  
1. .610  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
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ORIGIN  
Alignment Scores:  
Pred. No.: 1.66e-66 Length: 610  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
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Qy 1 PheAlaValAlaGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20  
Db 86 TTTCCTGTAGAAAATCCCATATATGACTGTGGCAGAGACCTTGACACTCTCTCCACT 145  
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40  
Db 146 CATGAACTGGCTGATAGGCGATGGGAACTGATGATTCCTACTCTGAAAATRAAAAT 205  
Qy 41 HisGlnLeuCySileuVgIuValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
Db 206 CACCAACTGGCATTAAGAAGTTTTCAGGGTATGACACATTAAGAAGCAAACTGCC 265  
Qy 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80  
Db 266 CACGGGAGGCTGGATTAACATATTCCTCAAACTTGTCTTTAATTAAGAAGCAATAGAG 325  
Qy 81 ArgGlnLysLysArgCySAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100  
Db 326 CGCCAAAAGAGCTGGATTAACATATTCCTCAAACTTGTCTTTAATTAAGAAGCAATAGAG 385  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 386 CAAATATTTCTTGGTGTATTAACACCGAGTGAACCGGAAAGT 430  
RESULT 15  
BD211559 610 bp DNA linear PAT 17-JUN-2003  
LOCUS Canine and feline immunoregulatory proteins, nucleic acid molecules  
DEFINITION and method of using the same.  
ACCESSION BD211559  
VERSION BD211559.1 GI:33021329  
KEYWORDS JP 2002516104-A/65.  
SOURCE Canis familiaris (dog)

## ORGANISM

Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

## REFERENCE

1 (bases 1 to 610)

## AUTHORS

Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.

## TITLES

Canine and feline immunoregulatory proteins, nucleic acid molecules

## JOURNAL

Patent: JP 2002516104-A 65 04-JUN-2002;

## COMMENT

HESKA CORP

## OS

Canis familiaris (dog)

## PN

JP 2002516104-A/65

## PD

04-JUN-2002

## PF

28-MAY-1999 JP 2000551002

## PI

29-MAY-1998 US 60/087306

## PR

GREKCEB SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC

## PC

C12N15/09,A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,

## PC

A61K39/395

## PC

A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,

## PC

C07K14/54,

## PC

C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC

## G01N33/15,

## PC

G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine

## and feline immunoregulatory proteins, nucleic acid CC

## molecules and

## CC

method of using the same

## FH

Key Location/Qualifiers

## FT

source 1..610 /organism='Canis familiaris (dog)'

## FEATURES

## source

## 1..610

## /organism='Canis familiaris'

## /mol\_type='genomic DNA'

## /db\_xref='taxon:9615'

## ORIGIN

## Alignment Scores:

## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

## US-10-787-382-10 (1-115) x BD211559 (1-610)

## Qy

## Db

## Qy

## Db

## Qy

## Db

## Qy

## Db

## Qy

## Db

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## Qy

## Db

## Qy

## Db

## Qy

## Db

Search completed: August 6, 2005, 22:43:07

Job time : 2113.1 secs



GenCore version 5.1.6  
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OW protein - nucleic search, using frame\_p2n model

Run on: August 6, 2005, 19:27:15 ; Search time 314.518 Seconds

(without alignments)  
2164.487 Million cell updates/sec

Title: US-10-787-382-10

Perfect score: 610

Sequence: 1 FAVENPMNRVAVETLTLLST.....FLDYLGVLGVINTWTPES 115

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool\_p/US10787382/runat\_04082005\_084751\_19282/apd\_query.fasta\_1.590  
-DB=N\_Geneseq\_16dec04 -OPMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query	Score	Match length	ID	Description
1	610	100.0	345	AAZ55550	Canine ma
2	610	100.0	345	AAZ55551	Canine ma
3	610	100.0	402	AAZ55548	Canine in
4	610	100.0	402	AAZ55549	Canine in
5	610	100.0	610	AAZ55546	Canine in

C	6	610	100.0	610	3	AAZ55547	AAZ55547 Canine in
	7	601	98.5	405	4	AAZ55548	AAZ55548 Canine in
	8	513	84.1	393	4	AAZ55549	AAZ55549 Canine in
	9	510	83.6	838	3	AAZ55550	AAZ55550 Canine in
	10	487	79.8	339	2	AAZ55551	AAZ55551 Canine in
	11	487	79.8	520	2	AAZ55552	AAZ55552 Canine in
	12	361	59.2	370	1	AAZ55553	AAZ55553 Canine in
	13	357	58.5	864	9	AAZ55554	AAZ55554 Canine in
	14	356	58.4	816	3	AAZ55555	AAZ55555 Canine in
	15	356	58.4	816	3	AAZ55556	AAZ55556 Canine in
	16	356	58.4	816	3	AAZ55557	AAZ55557 Canine in
	17	356	58.4	816	10	AAZ55558	AAZ55558 Canine in
	18	356	58.4	816	10	AAZ55559	AAZ55559 Canine in
	19	356	58.4	816	13	AAZ55560	AAZ55560 Canine in
	20	356	58.4	816	13	AAZ55561	AAZ55561 Canine in
	21	356	58.4	816	9	AAZ55562	AAZ55562 Canine in
	22	356	58.4	816	9	AAZ55563	AAZ55563 Canine in
	23	356	58.4	816	9	AAZ55564	AAZ55564 Canine in
	24	356	58.4	816	3	AAZ55565	AAZ55565 Canine in
	25	356	58.4	816	3	AAZ55566	AAZ55566 Canine in
	26	356	58.4	816	10	AAZ55567	AAZ55567 Canine in
	27	356	58.4	816	10	AAZ55568	AAZ55568 Canine in
	28	356	58.4	816	11	AAZ55569	AAZ55569 Canine in
	29	351	57.5	377	2	AAZ55570	AAZ55570 Canine in
	30	350	57.4	816	11	AAZ55571	AAZ55571 Canine in
	31	347	56.9	348	2	AAZ55572	AAZ55572 Canine in
	32	347	56.9	399	2	AAZ55573	AAZ55573 Canine in
	33	347	56.9	402	2	AAZ55574	AAZ55574 Canine in
	34	347	56.9	1533	1	AAZ55575	AAZ55575 Canine in
	35	347	56.9	1534	2	AAZ55576	AAZ55576 Canine in
	36	347	56.9	1623	2	AAZ55577	AAZ55577 Canine in
	37	347	56.9	1623	2	AAZ55578	AAZ55578 Canine in
	38	346	56.7	402	1	AAZ55579	AAZ55579 Canine in
	39	343	56.2	252	4	AAZ55580	AAZ55580 Canine in
	40	343	56.2	342	2	AAZ55581	AAZ55581 Canine in
	41	342	56.1	339	2	AAZ55582	AAZ55582 Canine in
	42	332.5	54.5	381	3	AAZ55583	AAZ55583 Canine in
	43	332	54.4	1945	10	AAZ55584	AAZ55584 Canine in
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	45	330.5	54.2	375	3	AAZ55586	AAZ55586 Canine in

# ALIGNMENTS

RESULT 1	AAZ55550	AAZ55550 standard; cDNA; 345 BP.
XX	AAZ55550;	
AC	AAZ55550;	
XX	14-MAR-2000 (first entry)	
DT	14-MAR-2000 (first entry)	
XX	Canine mature Interleukin-5 (IL-5) cDNA.	
DE	Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;	
XX	immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.	
XX	Canis familiaris.	
OS	Canis familiaris.	
XX	MO9961618-A2.	
PN	MO9961618-A2.	
XX	02-DEC-1999.	
PD	02-DEC-1999.	
XX	28-MAY-1999; 99WC-US011942.	
PP	28-MAY-1999; 99WC-US011942.	
XX	29-MAY-1998; 98US-0087306P.	
PR	29-MAY-1998; 98US-0087306P.	
XX	(HESK-) HESKA CORP.	
PA	(HESK-) HESKA CORP.	
XX	Sim G, Yang S, Dreitz MJ, Wonderling RS;	
FI	WPI; 2000-072623/06.	
XX	WPI; 2000-072623/06.	
DR	P-PSDB; AAY58220.	

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease.  
XX  
XX  
PS Claim 1b, Page 226-227, 264pp; English.  
XX  
XX Sequences AA255546-Z55551 represent cDNA sequences encoding canine  
CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
CC feline IL-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha),  
CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
CC nucleotides which encode these immunoregulatory proteins. The proteins,  
CC their associated nucleic acids, specific antibodies and inhibitors may be  
CC used as vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans). They  
CC may be used to treat autoimmune or infectious diseases including  
CC allergies, tumors, inflammation and graft rejection, and to increase the  
CC response from a co-administered antigen. The nucleotide sequences can  
CC also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for modulators  
CC of activity, while the antibodies may be used in detection, and in drug  
CC targeting  
XX  
SQ Sequence 345 BP, 120 A, 68 C, 78 G, 79 T, 0 U, 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 5, 61e-70 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 3  
US-10-787-382-10 (1-115) x AA255550 (1-345)  
QY 1 PheAlaValGluAnpProweTAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 1 TTGGCTGTAGAAATCCCATGAATAGACTGGTGCAGAGACCTTGACACGCTCTCCACT 60  
QY 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsn 40  
Db 61 CATCGAAGCTGGCTGATAGGCGATGGAGACCTGATGATCTTCTTCTGAAAAATAAAAAT 120  
QY 41 HisGlnLeuCyHisLeuGluValPheGlnGlyIleAspThrLeuLeuAsnGlnThrAla 60  
Db 121 CACCACTGTGCAATTAAAGAGTTTTCAGGATATAGACATTTGAAGAACCAACTGCC 180  
QY 61 HisGlyGluAlaValAspLeuPheGlnAsnLeuSerLeuIleGlyGluHisIleGlu 80  
Db 181 CACGGGAGGCTGTGATTAACATTTCCAAAACCTGTCTTAAATAAAGAACCATAGAG 240  
QY 81 ArgGlnLeuValAspGlyValGlyGluArgTrpArgValThrLeuPheLeuAspTrpLeu 100  
Db 241 CGCCAAAAAAGAGTGTGCGAGGAAAGATGAGAGTGAACAAAGTTCTAGACTACTG 300  
QY 101 GluValPheLeuGluValIleAsnThrGluTrpThrProGluSer 115  
Db 301 CAAATATTTCTGTGTATTAACACCGAGTGAACCGGAGAACT 345  
RESULT 2  
AA255551/c  
ID AA255551 standard; cDNA, 345 BP.  
XX  
XX AA255551;  
XX  
XX 14-MAR-2000 (first entry)  
XX  
XX Canine mature interleukin-5 (IL-5) cDNA complement.  
XX  
XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX  
OS Canis familiaris.  
XX  
XX WO961618-A2.  
XX  
XX  
XX 02-DEC-1999.  
XX  
XX 28-MAY-1999; 99WO-US011942.  
XX  
XX 29-MAY-1998; 98US-0087306P.  
XX  
XX (HESKA) HESKA CORP.  
XX  
XX Sim G, Yang S, Dretz MJ, Wonderling RS;  
XX WPI; 2000-072623/06.  
XX P-PADB; AAY58220.  
XX  
XX  
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease.  
XX  
XX  
PS Claim 1b, Page 228; 264pp; English.  
XX  
XX Sequences AA255546-Z55551 represent cDNA sequences encoding canine  
CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
CC feline IL-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha),  
CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
CC nucleotides which encode these immunoregulatory proteins. The proteins,  
CC their associated nucleic acids, specific antibodies and inhibitors may be  
CC used as vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans). They  
CC may be used to treat autoimmune or infectious diseases including  
CC allergies, tumors, inflammation and graft rejection, and to increase the  
CC response from a co-administered antigen. The nucleotide sequences can  
CC also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for modulators  
CC of activity, while the antibodies may be used in detection, and in drug  
CC targeting  
XX  
SQ Sequence 345 BP, 79 A, 78 C, 68 G, 120 T, 0 U, 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 5, 61e-70 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 3  
US-10-787-382-10 (1-115) x AA255551 (1-345)  
QY 1 PheAlaValGluAnpProweTAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 345 TTGGCTGTAGAAATCCCATGAATAGACTGGTGCAGAGACCTTGACACGCTCTCCACT 286  
QY 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsn 40  
Db 285 CATCGAAGCTGGCTGATAGGCGATGGAGACCTGATGATCTTCTTCTGAAAAATAAAAAT 226  
QY 41 HisGlnLeuCyHisLeuGluValPheGlnGlyIleAspThrLeuLeuAsnGlnThrAla 60  
Db 225 CACCACTGTGCAATTAAAGAGTTTTCAGGATATAGACATTTGAAGAACCAACTGCC 166  
QY 61 HisGlyGluAlaValAspLeuPheGlnAsnLeuSerLeuIleGlyGluHisIleGlu 80  
Db 165 CACGGGAGGCTGTGATTAACATTTCCAAAACCTGTCTTAAATAAAGAACCATAGAG 106  
QY 81 ArgGlnLeuValAspGlyValGlyGluArgTrpArgValThrLeuPheLeuAspTrpLeu 100  
Db 105 CGCCAAAAAAGAGTGTGCGAGGAAAGATGAGAGTGAACAAAGTTCTAGACTACTG 46

```
OY      101  GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
DB      45  CAAATATTCTTGCTGTAATTAACCCGAGTGACACCGGAAAGT 1
RESULT 3
ID      AA255548
XX      AA255548 standard; cDNA; 402 BP.
AC      AA255548;
XX      14-MAR-2000 (first entry)
DT
XX      Canine interleukin-5 (IL-5) cDNA coding region.
DE
XX      Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW      immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
XX      Canis familiaris.
OS
XX      WO9961618-A2.
XX      02-DEC-1999.
XX      28-MAY-1999; 99WO-US011942.
XX      29-MAY-1998; 98US-0087306P.
XX      (HESK-) HESKA CORP.
XX      Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX      WPI; 2000-072623/06.
XX      P-PSDB; AAY58219.
XX      Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT      useful for treating or preventing e.g. tumors or autoimmune disease.
XX      Claim 1h; Page 225; 264pp; English.
XX
XX      Sequences AA255546-255551 represent cDNA sequences encoding canine
CC      interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
CC      feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
CC      ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
CC      and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
CC      nucleotides which encode these immunoregulatory proteins. The proteins,
CC      their associated nucleic acids, specific antibodies and inhibitors may be
CC      used as vaccines for therapeutic or prophylactic regulation of an immune
CC      response in animals (particularly cats, dogs, horses and humans). They
CC      may be used to treat autoimmune or infectious diseases including
CC      allergies, tumours, inflammation and graft rejection, and to increase the
CC      response from a co-administered antigen. The nucleotide sequences can
CC      also be used for the recombinant production of a protein, while
CC      nucleotide fragments are useful as probes, as amplification primers and
CC      as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC      The proteins may be used to raise antibodies and to screen for modulators
CC      of activity, while the antibodies may be used in detection, and in drug
CC      targeting.
XX
XX      Sequence 402 BP; 129 A; 79 C; 93 G; 101 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 6.94e-70 Length: 402
Score: 610.00 Matches: 115
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-787-382-10 (1-115) x AA255548 (1-402)
OY      1  PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20
|||||
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```
DB      58  TTGCTGTAGAAAATCCCATGAATAGACTGTGCAGAGACTTGACACTGCTCCACT 117
OY      21  HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
DB      118  CATGGAACCTTGCTGATAGGCGATGGGAACTGATGATTCCTCTACTCGTAAAAATAAAT 177
OY      41  HisGlnLeuCyHisIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60
DB      178  CACCACTGTGCTTAAGAAAGTTTTCAGGGTATAGACATTTGAAACCAAACTGCCC 237
OY      61  HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
DB      238  CACGGGAGGCTGTGATTAACCTATTCGCAAACTTGCTTTAATTAAGAACACATAGAG 297
OY      81  ArgGlnLysLysArgCysAlaIleGlyLysArgTrpArgValThrLysPheLeuAspTrpLeu 100
DB      298  CGCCAAAAAAGAGTGTGAGGAAAGATGAGAGTGCAGAAAGTTCTTAAGTACTACCTG 357
OY      101  GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
DB      358  CAAATATTCTTGCTGTAATTAACCCGAGTGACACCGGAAAGT 402
RESULT 4
ID      AA255549/c
XX      AA255549 standard; cDNA; 402 BP.
XX      AA255549;
XX      14-MAR-2000 (first entry)
XX      Canine interleukin-5 (IL-5) cDNA coding region complement.
DE
XX      Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW      immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX      Canis familiaris.
OS
XX      WO9961618-A2.
XX      02-DEC-1999.
XX      28-MAY-1999; 99WO-US011942.
XX      29-MAY-1998; 98US-0087306P.
XX      (HESK-) HESKA CORP.
XX      Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX      WPI; 2000-072623/06.
XX      P-PSDB; AAY58219.
XX      Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT      useful for treating or preventing e.g. tumors or autoimmune disease.
XX      Claim 1h; Page 226; 264pp; English.
XX
XX      Sequences AA255546-255551 represent cDNA sequences encoding canine
CC      interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
CC      feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
CC      ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
CC      and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
CC      nucleotides which encode these immunoregulatory proteins. The proteins,
CC      their associated nucleic acids, specific antibodies and inhibitors may be
CC      used as vaccines for therapeutic or prophylactic regulation of an immune
CC      response in animals (particularly cats, dogs, horses and humans). They
CC      may be used to treat autoimmune or infectious diseases including
CC      allergies, tumours, inflammation and graft rejection, and to increase the
CC      response from a co-administered antigen. The nucleotide sequences can
CC      also be used for the recombinant production of a protein, while
CC      nucleotide fragments are useful as probes, as amplification primers and
CC      as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC      The proteins may be used to raise antibodies and to screen for modulators
```

CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting  
 XX  
 SQ Sequence 402 BP; 101 A; 93 C; 79 G; 129 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 6,94e-70 Length: 402  
 Score: 610.00 Matches: 115  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-10-787-382-10 (1-115) x AA255549 (1-402)

Qy 1 PheAlaValGluAenPromeAaArgLeuValAlaGluThrLeuThrLeuSerThr 20  
 Db 345 TTGCTGTAGAAATCCCATGAAATAGACTGTGGCAGAGACCTTGACATGCTCTCCACT 286  
 Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleAsn 40  
 Db 285 CATGAACCTTGCTGATAGGCGATGGGAACTGATGATTCCTACTCCTGAAAAATAAAT 226  
 Qy 41 HisGlnLeuCylielysGluValPheGlnGlyIleAspThrLeuIleAsnGlnThrAla 60  
 Db 225 CACCACTGTGCATTAAAGAGTTTTCAGGGTATAGACATTGAAGAAACCAAACTGCC 166  
 Qy 61 HisGlnGluAlaValAspIleuPheGlnAsnLeuSerLeuIleGluHisIleGlu 80  
 Db 165 CACGGGAGGCTGTGATTAACATATCCCAAACTGTCTTAAATAAAGAACATAGAG 106  
 Qy 81 ArgGlnIleuIleAspGlyAsnGlyGluArgTrpArgValThrIlePheLeuAspTrpLeu 100  
 Db 105 CGCCAAAAAAGAGTGTGGCAGGAGAAAGATGAGAGTGAAGTTCTTAGACTACTG 46  
 Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
 Db 45 CAAGTATTTCTTGCTGTATTAACACCGAGTGAACCGGAAAGT 1

## RESULT 5

AA255546 standard; cDNA; 610 BP.

AC AA255546;

DT 14-MAR-2000 (first entry)

DB Canine interleukin-5 (IL-5) cDNA.

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

OS Canis familiaris.

XX Key Location/Qualifiers

PH CD8 29.433

FT /\*tag= a

PN /product= "Canine IL-5"

XX MO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US011942.

XX 29-MAY-1998; 98US-0087306P.

XX (HESK-) HESKA CORP.

XX SIm G, Yang S, Drelitz MJ, Wonderling RS;  
 DR WPI; 2000-072623/06.  
 DR P-PSDB; AAY58219.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
 PT useful for treating or preventing e.g. tumors or autoimmune disease.  
 XX  
 XX Claim 1b; Page 223-224; 264pp; English.

XX Sequences AA255546-255551 represent cDNA sequences encoding canine  
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD134 (CD40  
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
 CC nucleotides which encode these immunoregulatory proteins. The proteins,  
 CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting

SQ Sequence 610 BP; 202 A; 114 C; 139 G; 155 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.24e-69 Length: 610  
 Score: 610.00 Matches: 115  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-10-787-382-10 (1-115) x AA255546 (1-610)

Qy 1 PheAlaValGluAenPromeAaArgLeuValAlaGluThrLeuThrLeuSerThr 20  
 Db 86 TTGCTGTAGAAATCCCATGAAATAGACTGTGGCAGAGACCTTGACATGCTCTCCACT 145  
 Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleAsn 40  
 Db 146 CATGAACCTTGCTGATAGGCGATGGGAACTGATGATTCCTACTCCTGAAAAATAAAT 205  
 Qy 41 HisGlnLeuCylielysGluValPheGlnGlyIleAspThrLeuIleAsnGlnThrAla 60  
 Db 206 CACCACTGTGCATTAAAGAGTTTTCAGGGTATAGACATTGAAGAAACCAAACTGCC 265  
 Qy 61 HisGlnGluAlaValAspIleuPheGlnAsnLeuSerLeuIleGluHisIleGlu 80  
 Db 266 CACGGGAGGCTGTGATTAACATATCCCAAACTGTCTTAAATAAAGAACATAGAG 325  
 Qy 81 ArgGlnIleuIleAspGlyAsnGlyGluArgTrpArgValThrIlePheLeuAspTrpLeu 100  
 Db 326 CGCCAAAAAAGAGTGTGGCAGGAGAAAGATGAGACTGCAAAAGTTCTTAGACTACTG 385  
 Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
 Db 386 CAAGTATTTCTTGCTGTATTAACACCGAGTGAACCGGAAAGT 430

## RESULT 6

AA255547/c standard; cDNA; 610 BP.

AC AA255547;

DT 14-MAR-2000 (first entry)

DB Canine interleukin-5 (IL-5) cDNA complement.

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

Key	Location/Qualifiers
Canis familiaris.	
Key	Location/Qualifiers
FT CDS	complement (178, .582)
FT	/tag= a
FT	/product= "Canine IL-5"
PN	W09961618-A2.
PD	02-DEC-1999.
PF	28-MAY-1999; 99WO-US011942.
PR	29-MAY-1999; 98US-0087306P.
PA	(HESK-) HESKA CORP.
PI	Sim G, Yang S, Dreitz MJ, Wonderling RS;
DR	WPI; 2000-072623/06.
DR	P-PSDB; AAY58219.
XX	Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX	useful for treating or preventing e.g. tumors or autoimmune disease.
XX	Claim 1h; Page 224-225; 264pp; English.
XX	Sequences AA255546-255551 represent cDNA sequences encoding canine
XX	interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
XX	canine Flt-3 ligand, canine or feline CD40, canine or feline CD134 (CD40
XX	ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
XX	and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
XX	nucleotides which encode these immunoregulatory proteins. The proteins,
XX	their associated nucleic acids, specific antibodies and inhibitors may be
XX	used as vaccines for therapeutic or prophylactic regulation of an immune
XX	response in animals (particularly cats, dogs, horses and humans). They
XX	may be used to treat autoimmune or infectious diseases including
XX	allergies, tumours, inflammation and graft rejection, and to increase the
XX	response from a co-administered antigen. The nucleotide sequences can
XX	also be used for the recombinant production of a protein, while
XX	nucleotide fragments are useful as probes, as amplification primers and
XX	as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX	The proteins may be used to raise antibodies and to screen for modulators
XX	of activity, while the antibodies may be used in detection, and in drug
XX	targeting
XX	Sequence 610 BP; 155 A; 139 C; 114 G; 202 T; 0 U; 0 Other;
XX	Alignment Scores:
XX	Pred. No.: 1,24e-69 Length: 610
XX	Score: 610.00 Matches: 115
XX	Percent Similarity: 100.00% Conservative: 0
XX	Best Local Similarity: 100.00% Mismatch: 0
XX	Query Match: 100.00% Indels: 0
XX	DB: 3 Gaps: 0
XX	US-10-787-382-10 (1-115) x AA255547 (1-610)
QY	1 PhealavalalualuasnPrometCAsnaAGLeuValalaglThrleuThrleuLeuSerThr 20
Db	525 TTGGCTGTAGAAATCCATGATATACATCTGTGGCAGAGACCTTGACACCTGCTCCAC 466
QY	21 HlbaTgThTTPleuileglYaspGlyasnLeuMetileProThrProGluasnlyPasn 40
Db	465 CATCGAACTTGCTGTATAGCCGATGGGAACCTGATATCTCTCTCTCTGAAAAATTA 406
QY	41 HlsglntleuCyelileYegluValIPreglNGlyleAspThrleuYsaAnglntRala 60
Db	405 CACCAACTGTGCTTTAAAGAGTTTTCACGGGATATGACACATTGAAGAACCAACTGCC 346
QY	61 HlsglYglualavalasplyleuPheglInasnleuSerleuileYsglunlslleglu 80

Db	345	CACGGGAGAGCTGTGATTAATCTATTCCAAACCTGCTTTTAATATAAAGACATRAG	288
Qy	81	ArgintylsaryGysalaglygiuargtPargValThrlysbheueaPryrleu	100
Db	285	CGCCAAAAAAGGtGTGCAGAGAAAGATGAGAGTGAACAAAGTTCTAGACTACTG	226
Qy	101	GlnValPheleuglyVallleaThrlytPThrProgluSer	115
Db	225	CAAGTATTTCTGTGTATATAAACCGGAGTGACACCGGAAGT	181
RESULT 7			
AAAF74300			
ID	AAAF74300	standard; DNA; 405 BP.	
XX			
AC	AAAF74300;		
XX			
DT	04-MAY-2001	(first entry)	
XX			
DE	Canine interleukin-5 coding sequence #1.		
XX			
KW	Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;		
KM	inflammatory reaction; ds.		
XX			
OS	Canis sp.		
XX			
PN	WO200111049-A2.		
XX			
PD	15-FEB-2001.		
XX			
PF	09-AUG-2000; 2000MO-US021651.		
XX			
PR	10-AUG-1999; 99US-00371615.		
XX			
PA	(INDEX-) IDEXX LAB INC.		
XX			
PI	Guo H, Lawton R, Nermer B, Aiyappa AP;		
XX			
DR	WPI; 2001-191542/19.		
XX			
DR	P-PSDB; AAB72615.		
XX			
PT	Novel canine interleukin 5 polynucleotide and polypeptides are used for		
XX	generating antibodies which are useful in treating allergies in dogs.		
PS	Claim 31; Page 46; 48pp; English.		
XX			
CC	The present invention provides the protein and coding sequences of the		
CC	canine interleukin-5 (IL-5) protein. This can be used to treat allergies,		
CC	cancer and inflammatory reactions in dogs. The present sequence is one		
CC	version of the IL-5 coding sequence shown in the specification		
XX			
SQ	Sequence 405 BP; 131 A; 77 C; 94 G; 103 T; 0 U; 0 Other;		
Alignment Scores:			
	Pred. No.:	1,046-68	Length: 405
	Score:	601.00	Matches: 114
	Percent Similarity:	99.13%	Conservative: 0
	Best Local Similarity:	99.13%	Mismatches: 1
	Query Match:	98.52%	Indels: 0
DB:		4	Gaps: 0
US-10-787-382-10 (1-115) x AAF74300 (1-405)			
Qy	1	PhealaValGluAnPromeFasbnrgleuValAlaGluThrleuThrleuSerThr	20
Db	58	TTGTGCTGAGAAATCCCATGAATGACTGTGGCAGAGACCTTGACACTGCTCCACT	117
Qy	21	HIsAcGTTrTPLeuileGlyAspGlyAnleuMetileProThrProGlubnlyAsn	40
Db	118	CATCAACTGTGCTGATRAGCGCATGGGAACCTGATATTCCTAAGATAAATAAAT	177
Qy	41	HIsGlnLeuCyelleyeGluValPheGnglylleAspThrleuLyAsnglnThrala	60
Db	178	CACCAACTGTGATTAAGAGCTTTTTCGGGCTATRAGACATTTGAAAGAACCAACTGCC	237

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Qy 61 HieglYgIuAlaValaAspLysLeuPheGlnAsnLeuSerLeuIleYsgIuHieglu 80
Db 238 CAGGGGAGGCTGCTGATTAACCTATTCACAAACTGCTTTAATAAAGAACATAGAG 237
Qy 81 ArgGlnLysLysArgCysAlaGlyGlnArgTrpArgValThrLysPheLeuAspTrpLeu 100
Db 298 CGCCAAAATAAAGAGTGTGACGAGAAAGATGAGAGTGTGACAAAGTTCTTACACTACCTG 357
Qy 101 GlnValPheLeuGlyValIleAsnThrGlnTrpThrProGlnSer 115
Db 358 CAAGTATTCTTGCTGCTGATTAACCCGAGTGTGACAAATGGAAGT 402

RESULT 8
AA74306
ID AA74306 standard; DNA; 393 BP.
AC AA74306;
NC
NT
DT 04-MAY-2001 (first entry)
DE Canine Interleukin-5 coding sequence #3.
DX
XX Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
XX Inflammatory reaction; ds.
XX
XX Canis sp.
XX
XX WO200111049-A2.
XX
XX 15-FEB-2001.
XX
XX 09-AUG-2000; 2000WO-US021651.
XX
XX 10-AUG-1999; 99US-00371615.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Guo H, Lawton R, Mermer B, Aiyappa AP;
XX WPI; 2001-191542/19.
XX
XX Novel canine interleukin 5 polynucleotide and polypeptides are used for
XX generating antibodies which are useful in treating allergies in dogs.
XX
XX Claim 1; Page 35; 48pp; English.
XX
XX The present invention provides the protein and coding sequences of the
XX canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
XX cancer and inflammatory reactions in dogs. The present sequence is one
XX version of the IL-5 coding sequence shown in the specification
XX
XX Sequence 393 BP; 128 A; 82 C; 86 G; 97 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,94e-57 Length: 393
Score: 513.00 Matches: 95
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 97.94% Mismatches: 0
Query Match: 84.10% Indels: 0
Gaps: 0
DB: 4

US-10-787-382-10 (1-115) x AA74306 (1-393)

Qy 16 ThrLeuLeuSerThrHiegluArgTrpLeuIleGlnAspGlnLeuMetIleProThr 35
Db 1 ACACCTGCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 60
Qy 36 ProGlnLysLysAsnHiegluLeuCysIleYsgIuValPheGlnGlyIleAspThrLeu 55
Db 61 CCGTAAATAAATAATCAACCACTGTGATTAAGAAAGTTTTCAGGGATATGACACTTG 120
Qy 56 LysAsnGlnThrAlaHiegluAlaValaAspLysLeuPheGlnAsnLeuSerLeuIle 75
```

```
Db 121 AAGAACCAACTGCCACGGGGAGGCTGTGATAAATATTCACAAACTGCTTTAATA 180
Qy 76 LysGlnHiegluArgGlnLysArgCysAlaGlyGlnArgTrpArgValThrLys 95
Db 181 AAGAACCACTTAAGAGCCCAAAAATAAAGTGTGACGAGAAAGATGAGATGACAAAG 240
Qy 96 PheLeuAspTrpLeuGlnValPheLeuGlyValIleAsnThrGlnTrpThr 112
Db 241 TTCTTACACTACTGCAAGTATTCTTGCTCTATATAACACCGAGTGTGAGT 291

RESULT 9
AA244265
ID AA244265 standard; DNA; 838 BP.
AC AA244265;
NC
NT
DT 31-MAR-2000 (first entry)
DE Porcine IL-5 DNA.
DX
XX Pig; vaccine; cysticercosis; protective antigen; cC1; cC3; cC4;
XX tenial cysticercus; gamma interferon; IFN-gamma; interleukin 5; IL-5; ss.
XX
XX Sus scrofa.
XX
XX CN1231339-A.
XX
XX 13-OCT-1999.
XX
XX 29-JAN-1999; 99CN-00113447.
XX
XX 29-JAN-1999; 99CN-00113447.
XX
XX (UYTW-) UNIV NO 2 MILITARY MEDICAL PLA.
XX
XX Sun S, Dai J;
XX WPI; 2000-087904/08.
XX
XX Nucleic acid vaccine for cysticercosis co-contracted by human and pig.
XX
XX Claim 3; Page 9; 21pp; Chinese.
XX
XX This invention describes a novel nucleic acid vaccine for preventing and
XX curing human and pork cysticercosis. The invention involves the formation
XX of a eukaryotic expression plasmid from fusion transcript expression unit
XX consisting of three protective antigen genes (cC1, cC3 and cC4) of pig
XX tenial cysticercus and coexpression unit of related cell factor gamma
XX interferon (IFN-gamma) and pork interleukin 5 (IL-5) genes. The
XX production and purification process of said nucleic acid vaccine is
XX simple and convenient, the physical and chemical properties of the
XX vaccine are stable, and the vaccine is easy to store and transport, and
XX possesses effective immunological protective function for human and pig
XX cysticercosis. This sequence represents the pig IL-5 gene used in the
XX method of the invention
XX
XX Sequence 838 BP; 280 A; 148 C; 171 G; 239 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.07e-56 Length: 838
Score: 510.00 Matches: 96
Percent Similarity: 92.98% Conservative: 10
Best Local Similarity: 84.21% Mismatches: 8
Query Match: 83.61% Indels: 0
Gaps: 0
DB: 3

US-10-787-382-10 (1-115) x AA244265 (1-838)

Qy 2 AlaValGlnAsnProMetAsnArgLeuValAlaGlnThrLeuThrLeuSerThrHie 21
Db 105 GCTGTACAAAGTCCCATGAATAGGCTGTGTGACAGACCTTGGACACTGCTCTCCACTCAT 164
```

QY 22 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 41  
 Db 165 CGAACTCTACTGATAGGCGAGCACTGATGATCTTCTACTCTCGAACAATACATAC 224  
 QY 42 GlnLeuCySileYsgLvalPheGlnGlyIleAspThrLeuYsaGlnThrAlaHis 61  
 Db 225 CAACGTGTCATTGAAGAGTCTTTCAGGGTATAGACATTAAGATGCGACTGTGCG 284  
 QY 62 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleYsgLHisIleGluArg 81  
 Db 285 GGGGATGCTGTGGAAGAACTTTTCGAACTGTTTAATAAAGAACACATAGACCGC 344  
 QY 82 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 101  
 Db 345 CAAAGAAAAAGTGTGGAGGAGAGAGATGAGAGATTAAGAAAGTTCTTCTGACTTCTGCA 404  
 QY 102 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
 Db 405 GTGTTTCTGTGTATATTAACACTGAGTGCAGATGCAATGCAAGT 446  
 RESULT 10  
 AAT50756 standard; cDNA; 399 BP.  
 AAT50756:  
 AAT50756:  
 17-OCT-2003 (revised)  
 24-SEP-1997 (first entry)  
 DE Ovine IL-5 cDNA.  
 XX Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;  
 KW livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;  
 KM immunosuppression; allergy; reproductive system; growth; early maturity;  
 KM antibody; diagnosis; immunopotentiator;  
 KM early haematopoietic progenitor cell; cytotoxic cell; thymocyte;  
 KM secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.  
 XX Ovis aries.  
 OS WO9700321-A1.  
 PN 03-JAN-1997.  
 PD 14-JUN-1996; 96WO-AU000360.  
 PF 14-JUN-1995; 95AU-00003502.  
 PR 27-OCT-1995; 95AU-00006244.  
 XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 PA Seow H, Wood P;  
 PI WPI; 1997-07528/07.  
 DR P-PSDB; AAM08479.  
 XX Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine  
 PT adjuvants and to treat or prevent microbial infections in livestock.  
 XX Claim 6; Page 41-42; 78pp; English.  
 CC The sequences given in AAT50755-56 encode ovine interleukin-5 (IL-5).  
 CC Ovine IL-5 or IL-12 are used to treat and/or prevent infections in  
 CC livestock (esp. cows and sheep), particularly where the animals are  
 CC stressed, e.g. during transport. IL-5 and IL-12 can also be used as  
 CC adjuvants in vaccines for veterinary use (partic. weakly immunogenic  
 CC subunit or synthetic peptide vaccines). They may also be used to treat  
 CC cancer, immunosuppression and allergy, to enhance/suppress the  
 CC reproductive system and to promote growth or early maturity. Optionally  
 CC interleukin can be delivered from constructs or delivery cells and  
 CC antibodies are useful in enzyme immunoassays for rapid diagnosis of  
 CC infection. The interleukins are immunopotentiators, especially IL-5  
 CC promotes growth of early haematopoietic progenitor cells and generation

CC of cytotoxic cells from thymocytes, also it stimulates production and  
 CC secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12  
 CC induces production of gamma-interferon by, and proliferation of, T and NK  
 CC cells and increases the (non)-specific cytolytic lymphocyte response. The  
 CC genetic constructs can also be used for in vitro production of IL-5 or -  
 CC 12. (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 399 BP; 130 A; 77 C; 93 G; 99 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.34e-54 Length: 399  
 Score: 487.00 Matches: 92  
 Percent Similarity: 92.11% Conservative: 13  
 Best Local Similarity: 80.70% Mismatches: 9  
 Query Match: 79.84% Indels: 0  
 Db: 2 Gaps: 0  
 US-10-787-382-10 (1-115) x AAT50756 (1-399)  
 QY 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 21  
 Db 55 GCTGTAGAAAGTACCATGAAATAGACTGTGCGAGACCTTGACACTGCTCCACGCAAT 114  
 QY 22 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 41  
 Db 115 CAACCTCGCTGATAGGTGATGAGAACTTGATGATCTTCTACTCTCGACATCAAAATCAC 174  
 QY 42 GlnLeuCySileYsgLvalPheGlnGlyIleAspThrLeuYsaGlnThrAlaHis 61  
 Db 175 CAACATGATGATGGAAGAGTCTTTCAGGGATATAGACATTAAGAAATCAACATGCGCAA 234  
 QY 62 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleYsgLHisIleGluArg 81  
 Db 235 GGGGATGCTGTGGAAGAACTTTTCGAACTGTTTAATAAAGAACATACATAGACCTC 294  
 QY 82 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 101  
 Db 295 CAAAGAAAAAGTGTGGAGGAGAGAGATGAGAGATTAAGAAAGTTCTTCTGACTTCTGCA 354  
 QY 102 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
 Db 355 GTTTCCTGTGTGTATTAACACAGATGAGTGAAGAAAGC 396  
 RESULT 11  
 AAT50755 standard; DNA; 520 BP.  
 AAT50755:  
 AAT50755:  
 17-OCT-2003 (revised)  
 24-SEP-1997 (first entry)  
 DE Ovine IL-5 gene.  
 XX Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;  
 KW livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;  
 KM immunosuppression; allergy; reproductive system; growth; early maturity;  
 KM antibody; diagnosis; immunopotentiator;  
 KM early haematopoietic progenitor cell; cytotoxic cell; thymocyte;  
 KM secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.  
 XX Ovis aries.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 46..444  
 FT /\*tag= a  
 FT /product= "Ovine\_IL-5"  
 FT exon 46..183  
 FT /\*tag= b  
 FT /number= 1  
 FT exon 184..216  
 FT /\*tag= c  
 FT /number= 2

```
FT      exon                217..345
FT      /*tag= d
FT      /number= 3
FT      exon                346..480
FT      /*tag= e
FT      /number= 4
XX      MO9700321-A1.
XX      03-JAN-1997.
XX      14-JUN-1996; 96MO-AU000360.
XX      14-JUN-1995; 95AU-00003502.
XX      27-OCT-1995; 95AU-00006244.
XX      (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX      Seow H, Wood P;
XX      WPI; 1997-077528/07.
XX      P-PSDB; AAM08479.
XX      Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
XX      adjuvants and to treat or prevent microbial infections in livestock.
XX      Claim 6; Page 39-40; 78pp; English.
XX      The sequences given in AAT50755-56 encode ovine interleukin-5 (IL-5).
XX      Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
XX      livestock (esp. cows and sheep), particularly where the animals are
XX      stressed, e.g. during transport. IL-5 and IL-12 can also be used as
XX      adjuvants in vaccines for veterinary use (partic. weakly immunogenic
XX      subunit or synthetic peptide vaccines). They may also be used to treat
XX      cancer, immunosuppression and allergy, to enhance/suppress the
XX      reproductive system and to promote growth or early maturity. Optionally
XX      interleukin can be delivered from constructs or delivery cells and
XX      antibodies are useful in enzyme immunoassays for rapid diagnosis of
XX      infection. The interleukins are immunopotentiators, especially IL-5
XX      promotes growth of early haematopoietic progenitor cells and generation
XX      of cytotoxic cells from thymocytes, also it stimulates production and
XX      secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
XX      induces production of gamma-interferon by, and proliferation of, T and NK
XX      cells and increases the (non-specific cytolytic lymphocyte response. The
XX      genetic constructs can also be used for in vitro production of IL-5 or -
XX      12. (Updated on 17-OCT-2003 to standardise OS field)
SQ      Sequence 520 BP; 166 A; 99 C; 124 G; 131 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1,06e-53 Length: 520
Score: 487.00 Matches: 92
Percent Similarity: 92.11% Conservative: 13
Best Local Similarity: 80.70% Mismatches: 9
Query Match: 79.84% Indels: 0
Gaps: 0
DB: 2
US-10-787-382-10 (1-115) x AAT50755 (1-520)
QY      2 A1AValGluAenProMetAenAryGluValAlaGluThrLeuThrLeuLeuSerThrHis 21
DB      100 GCTGTAGAAATACCATGAATAGACTGTGTGCAGAGACTTGACATCTCTCCACGCAT 159
QY      22 ArgThrTrpLeuIleGlyAAspGlyAAsnLeuMetIleProThrProGluAAsnIleAAsnHis 41
DB      160 CAAACCTGCTGATAGGTGATGGAACTTGATGATCTTACTCTCCAGCATACAAATCAC 219
QY      42 GlnLeuCyIeIyGluValAphGlnGlyIleAspThrLeuIyAAsnGlnThrAlaHis 61
DB      220 CAATATAGCATTTGAAGAAGTCTTTCAAGGAATAGACATTTGAAGAATCAACAGCCAA 279
QY      62 GlyIeIuAValAAspIyGluAAsnLeuSerLeuIleGlyGluHisIleGluArg 81
DB      111 GCTGTGCTGATAGGCAATAGACATCTCCGAGATCTGCTGATACAAAATCAC 130
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DB      280 GGGAGTGTGTGAAAAAAATATTCGAAACTGTCTTTAATAAAAAGATACATAGACTTC 339
QY      82 GlnIyelysArgCyAsnIleGlyIuAArgTrpAryValThrIySpheLeuAAspIyTrLeuGln 101
DB      340 CAAAAAGAAAGTGTGAGAGAAAGATGAGAGTGAACAATTCCTCCGACTACCTGCAA 399
QY      102 ValPheLeuGlyValIleAenThrGluTrpThrProGluSer 115
DB      400 GTTTCCTGTGTGATTAACACAGAGTGAAGCATGGAAGC 441
RESULT 12
AAN91647
ID      AAN91647 standard; DNA; 370 BP.
XX      AAN91647;
AC      AAN91647;
XX      25-MAR-2003 (revised)
DT      21-MAR-1990 (first entry)
XX      Synthetic interleukin-5 gene.
XX      Growth factor.
XX      Homo sapiens.
XX      Key Location/Qualifiers
XX      CDS 14..352
XX      /*tag= a
XX      GB2217328-A.
XX      25-OCT-1989.
XX      12-APR-1988; 88GB-00008524.
XX      12-APR-1988; 88GB-00008524.
XX      (BRBI-) BRITISH BIO-TECHN L.
XX      Edwards RM;
XX      WPI; 1989-311767/43.
XX      P-PSDB; AAP9152.
XX      Synthetic gene encoding human interleukin-5 - has restriction sites at
XX      frequent intervals to facilitate manipulation.
XX      Claim 1; Fig 3a; 21pp; English.
XX      Has sites for HindII, BspMI, NcoI, SpeI, BspMI, ApaLI, XbaI, XhoI ClaI,
XX      BclI, PciI, DraIII, BamHI and EcoRI. IL5 acts as a B cell growth and
XX      differentiation factor. (Updated on 25-MAR-2003 to correct PA field.)
SQ      Sequence 370 BP; 126 A; 73 C; 82 G; 89 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.74e-37 Length: 370
Score: 361.00 Matches: 71
Percent Similarity: 77.19% Conservative: 17
Best Local Similarity: 62.28% Mismatches: 26
Query Match: 59.18% Indels: 0
Gaps: 0
DB: 1
US-10-787-382-10 (1-115) x AAN91647 (1-370)
QY      2 A1AValGluAenProMetAenAryGluValAlaGluThrLeuThrLeuLeuSerThrHis 21
DB      11 GCAATGGAATATTCCTACTAGTGTGAAAGAGACTTGGACATGCTTTTACTCAT 70
QY      22 ArgThrTrpLeuIleGlyAAspGlyAAsnLeuMetIleProThrProGluAAsnIleAAsnHis 41
DB      71 CAAACCTGCTGATAGGCAATAGACATCTCCGAGATCTGCTGATACAAAATCAC 130
```



```
Qy 42 GlnLeuCySileuYsgluValPheGlnGlyIleAspThrLeuYsaenGlnThrAlaHis 61
Db 131 CAACTGTCACCTGAAGAAATCTTTCAGAGAAATAGGCACACTCGAGACTCAAACTGTGCA 190
Qy 62 GlnGluValAlaValPheGlnAsnLeuSerLeuIleYsgluHisIleGluArg 81
Db 191 GGGGGTACTGTGAAAGACTTATCAAAACTGTCTTAATTAAGAAATCATCATGATGCG 250
Qy 82 GlnLeuYsaenGlyCysAlaGlyGluArgTrpArgValThrYsaPheLeuAspTrpLeuGln 101
Db 251 CAAAGAAAAAGGTGTGAGAAAGAAACGAGAGATTAACCAATTCCTTACACTATCTGACG 310
Qy 102 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
Db 311 GAGTTCTTGCTGTAATGAACACCGAGTGGATTAATGAAGAT 352

RESULT 13
AAL61295 standard; DNA; 864 BP.
AC AAL61295;
DT 22-SEP-2003 (first entry)
XX
DB hIL5.36 variant DNA.
XX
KW Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;
KW tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;
KW IL5; epitope; human; tetanus toxoid; chimeric; variant; gene; ds.
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 1..864
FT /tag= a
FT /product= "hIL5.36 variant protein"
FT sig_peptide 1..57
FT /tag= b
FT /note= "Human IL5 leader peptide"
FT mat_peptide 58..861
FT /tag= c
FT /product= "Mature hIL5.36 variant protein"
FT misc_feature 70..132
FT /tag= d
FT /note= "Tetanus toxoid P30 epitope"
FT misc_feature 817..861
FT /tag= e
FT /note= "Tetanus toxoid P2 epitope"
XX
PN WO2003042244-A2.
XX
PD 22-MAY-2003.
XX
PR 15-NOV-2002; 2002KO-DK00764.
XX
PR 16-NOV-2001; 2001DK-00001702.
PR 16-NOV-2001; 2001US-0331575P.
XX
PA (PHAR-) PHARMEXA AS.
PA (KLYS-) KLYSNER S. S.
PA (NIEL-) NIELSEN F. S.
PA (BRAT-) BRATT T.
PA (VOLD-) VOLDORGB B.
PA (MOUR-) MOURITSEN S.
XX
PI Klysner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;
XX WPI; 2003-449558/42.
XX P-PSDB; AAO30459.
XX
PT New immunogenic analogue of a polymeric protein, useful for preparing a
```

```
PT composition for treating inflammatory diseases e.g. arthritis.
XX
PS Example 3; Page 114-115; 196pp; English.
XX
CC The invention relates to immunogenic analogues of multimeric proteins
CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic
CC analogues. The immunogenic analogue is useful for preparing a composition
CC for treating inflammatory diseases, e.g., arthritis. It is also used in
CC gene therapy. The present sequence is a variant DNA encoding a fusion
CC construct which comprises 2 human interleukin 5 (IL5) monomers joined by
CC diglycine linker and including terminally positioned tetanus toxoid
CC epitopes P30 and P2. This sequence is used to illustrate the method of
CC the invention
XX
SQ Sequence 864 BP; 278 A; 184 C; 201 G; 201 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.88e-36 Length: 864
Score: 357.00 Matches: 70
Percent Similarity: 76.99% Conservative: 17
Best Local Similarity: 61.95% Mismatches: 26
Query Match: 58.52% Indels: 0
DB: Gaps: 0

US-10-787-382-10 (1-115) x AAL61295 (1-864)
Qy 3 ValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHisArg 22
Db 127 CTGAGAGATTCCTCCACCAATGCAATGTGTGAAAGACCTTGGCACTCTTCTACTCATCGA 186
Qy 23 ThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnYsaenHisGln 42
Db 187 ACTGTGTAATAGCCAAATGAGACTCTGAGATTCCTGCTTCTGTAATTAATTAATCAACCA 246
Qy 43 LeuCySileuYsgluValPheGlnGlyIleAspThrLeuYsaenGlnThrAlaHisGly 62
Db 247 CTGTGACCTGAAGAAATCTTTCAGAGAAATAGGCACACTCGAGACTCAAACTGTGCAAGG 306
Qy 63 GlnValAlaValPheYsaenPheGlnAsnLeuSerLeuIleYsgluHisIleGluArg 82
Db 307 GGTACTGTGAAAGACTATTCAAAACTGTCTTAATTAAGAAATCATTCATGACGCGCA 366
Qy 83 LeuYsaenGlyCysAlaGlyGluArgTrpArgValThrYsaPheLeuAspTrpLeuGlnVal 102
Db 367 AAAAAAAGGTGTGAGAAAGAAACGAGAGATTAACCAATTCCTTACACTATCTGCAAGAG 426
Qy 103 PheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
Db 427 TTTCTTGCTGTAATGAACACCGAGTGGATTAATGAAGAT 465

RESULT 14
AAA34857 standard; DNA; 816 BP.
XX
AC AAA34857;
XX
DT 28-JUL-2000 (first entry)
XX
DB Human adenovine receptor related polynucleotide SEQ ID NO:2546.
XX
KW Human; adenovine receptor; low adenovine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiaesthetic; cytoskeletal; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
```

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XX 24-FEB-2000.
PD 03-AUG-1999; 99MO-US017712.
XX 03-AUG-1998; 98US-0095212P.
XX (UYEC-) UNIV EAST CAROLINA.
XX NYCE JW;
XX WPI; 2000-205971/18.
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX Disclosure; Page 716; 1343P; English.
XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have anti-inflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA3313 to AAA3512 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA3233 to
CC AAA3392) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
XX SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 2.34e-36 Length: 816
XX Score: 356.00 Matches: 70
XX Percent Similarity: 76.79% Conservative: 16
XX Best Local Similarity: 62.50% Mismatches: 26
XX Query Match: 58.36% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-10-787-382-10 (1-115) x AAA34857 (1-816)
XX
XX 4 GluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHisArgThr 23
XX 111 GAAATTCCTCCACAAATGCAATGCTGTAAGAGACCTTGACACTGCTTCTACTCATCGAAGCT 170
XX
XX 24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43
XX 171 CTGCTGATAGCAATGAGACTCTGAGAGATTCCTGCTTCTGACATAAAATACCAACTG 230
XX
XX 44 CysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHisGlyGlu 63
XX 231 TGCACTGAAGAAATCTTTCAGGAGATAGGCACACTGGAGAGTCAAACTGTGCAAGGGGT 290
XX
XX 64 AlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGlnHisGlnArgGlnLys 83
XX 291 ACTGTGAAAGACATTCACAAACTGTGCTTAATAAAGAAATACATTGACGGCCAAAAA 350
XX
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XX 84 LysArgCysAlaIleGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGlnValPhe 103
XX 351 AAAAAGTGTGGAAGAAAGAACGAGAGTAACCAATTCCTTAACCTACCTGCAAGACTTT 410
XX
XX 104 LeuGlyValIleAsnThrGluTrpThrProGlnSer 115
XX 411 CTGTGTATATGAACACCGAGTGGATATATGAAAGT 446
XX
XX RESULT 15
XX AAA13338
XX ID AAA13338 standard; cDNA; 816 BP.
XX
XX AAA13338;
XX
XX 25-JUL-2000 (first entry)
XX
XX Human interleukin-5 (IL-5) nucleotide sequence.
XX
XX Human; interleukin-5; IL-5; inflammatory disease; asthma; eczema;
XX antisense oligonucleotide; allergic rhinitis; inflammatory skin disease;
XX allergic conjunctivitis; inhibitor; ss.
XX
XX Homo sapiens.
XX
XX US6048726-A.
XX
XX 11-Apr-2000.
XX
XX 15-MAY-1998; 98US-00079839.
XX
XX 15-MAY-1998; 98US-00079839.
XX
XX (WEIT/) WELTMAN J K.
XX (KARI/) KARIM A S.
XX
XX WELTMAN JK, KARIM AS;
XX
XX WPI; 2000-302784/26.
XX
XX Oligonucleotide comprising non-natural internucleoside linkage, useful
XX for inhibiting interleukin-5 expression and treating inflammatory
XX diseases, asthma, allergic rhinitis, allergic conjunctivitis.
XX
XX Disclosure; Col 3-4; 11pp; English.
XX
XX This sequence represents the human interleukin-5 (IL-5) encoding
XX nucleotide sequence. Interleukin-5 is involved in eosinophilic
XX inflammation and inflammatory disorders. The present invention relates to
XX an IL-5 antisense oligonucleotide (see AAA13337) which inhibits the
XX expression of IL-5. The antisense oligonucleotide has at least one non-
XX natural internucleoside linkage. The oligonucleotide is able to inhibit
XX IL-5 secretion in a dose dependent manner and is useful for inhibiting
XX IL-5 expression and therefore treating inflammatory diseases, asthma,
XX allergic rhinitis, allergic conjunctivitis and inflammatory skin diseases
XX such as eczema
XX
XX SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 2.34e-36 Length: 816
XX Score: 356.00 Matches: 70
XX Percent Similarity: 76.79% Conservative: 16
XX Best Local Similarity: 62.50% Mismatches: 26
XX Query Match: 58.36% Indels: 0
XX DB: 3 Gaps: 0
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XX 111 GAAATTCCTCCACAAATGCAATGCTGTAAGAGACCTTGACACTGCTTCTACTCATCGAAGCT 170
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QY 24 TrpLeuIleGIyAepGIyAsnLeuMetIleProThrProGIuAAsnLyAsnHisGIuLeu 43
Db 171 CTGCTGATAGCCATAGAGACTCTGAGGATTCCTGCTGTAACATMAAAATCACCACTG 230
QY 44 CysIleLysGIuValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHisGIuGlu 63
Db 231 TGCACTGAAAGAAATCTTTCAGGGAATAGCACACTGAGAGACTCAAACTGTGCAAGGGGT 290
QY 64 AlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGIuHisIleGIuArgGlnLys 83
Db 291 ACTGTGAAAGACTAATCAAAACTTGTCTTAATAAGAAATACATTGACGGCCAAA 350
QY 84 LysArgCysAlaGIyGIuArgTrpArgValThrLysPheLeuAspTyrLeuGlnValPhe 103
Db 351 AAAAAGTGTGAGAAAGAAAGACGAGAGCTAAACCAATTCCTAGACTACTGCAAGAGTTT 410
QY 104 LeuGIyValIleAsnThrGIuTrpThrProGIuSer 115
Db 411 CTTGTGTAAATGAACACCGAGTGGATATATAGAAAGT 446

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Search completed: August 6, 2005, 21:26:46  
 Job time : 315.518 secs

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GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 6, 2005, 20:22:55 ; Search time 102.068 Seconds

(Without alignments)  
1843.588 Million cell updates/sec

Title: US-10-787-382-10

Perfect score: 610  
Sequence: 1 PAVBNPMNRVLAETLTLST.....FLDYLYQVFLGVINTEWTPES 115

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdd  
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## Database :

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3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
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5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	610	100.0	345	4	US-09-322-409-85
2	610	100.0	345	4	US-09-322-409-87
3	610	100.0	345	4	US-09-322-409-85
4	610	100.0	345	4	US-09-451-527-85
5	610	100.0	402	4	US-09-322-409-87
6	610	100.0	402	4	US-09-322-409-83
7	610	100.0	402	4	US-09-322-409-84
8	610	100.0	402	4	US-09-451-527-83
9	610	100.0	402	4	US-09-451-527-84
10	610	100.0	610	4	US-09-322-409-80
11	610	100.0	610	4	US-09-322-409-82
12	610	100.0	610	4	US-09-451-527-80
					Sequence 82, Appl

13	601	98.5	405	4	US-09-371-615A-1	Sequence 1, Appl1
14	356	58.4	816	3	US-09-079-839-2	Sequence 2, Appl1
15	351	57.5	377	3	US-09-180-864-1	Sequence 1, Appl1
16	350	57.4	816	4	US-09-023-655-1236	Sequence 1236, Ap
17	347	56.9	1534	3	US-08-629-643A-4	Sequence 4, Appl1
18	347	56.9	1534	3	US-09-155-884-4	Sequence 27, Appl1
19	332.5	54.5	381	4	US-09-556-818-39	Sequence 39, Appl1
20	331.5	54.3	399	4	US-09-556-818-37	Sequence 37, Appl1
21	330.5	54.2	375	4	US-09-556-818-33	Sequence 33, Appl1
22	328.5	53.9	393	4	US-09-556-818-31	Sequence 31, Appl1
23	324	53.1	444	4	US-09-556-818-43	Sequence 43, Appl1
24	322.5	52.9	393	4	US-09-556-818-41	Sequence 41, Appl1
25	321.5	52.7	375	4	US-09-556-818-37	Sequence 37, Appl1
26	319.5	52.4	375	4	US-09-556-818-45	Sequence 45, Appl1
27	318.5	52.2	393	4	US-09-556-818-55	Sequence 55, Appl1
28	315.5	51.7	387	4	US-09-556-818-49	Sequence 49, Appl1
29	311	51.0	438	4	US-09-556-818-59	Sequence 59, Appl1
30	309.5	50.7	387	4	US-09-556-818-57	Sequence 57, Appl1
31	308.5	50.6	369	4	US-09-556-818-53	Sequence 53, Appl1
32	301.5	49.4	357	4	US-09-556-818-35	Sequence 35, Appl1
33	289.5	49.1	375	4	US-09-556-818-29	Sequence 29, Appl1
34	289.5	47.5	351	4	US-09-556-818-51	Sequence 51, Appl1
35	287.5	47.1	369	4	US-09-556-818-47	Sequence 47, Appl1
36	222	36.4	6727	3	US-08-629-643A-5	Sequence 5, Appl1
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38	222	36.4	6727	3	US-09-280-799-78	Sequence 5, Appl1
39	215.5	35.3	3230	3	US-09-155-884-5	Sequence 78, Appl1
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41	215.5	35.3	3230	6	US-09-280-799-78	Sequence 78, Appl1
42	215.5	35.3	3230	6	US-09-280-799-78	Sequence 78, Appl1
43	76	12.5	33140	4	US-09-596-002-23	Sequence 23, Appl1
44	75	12.3	79595	4	US-09-949-016-15318	Sequence 23, Appl1
45	73	12.0	74353	4	US-09-949-016-12751	Sequence 15318, A
					US-09-949-016-15336	Sequence 15336, A

## ALIGNMENTS

RESULT 1  
US-09-322-409-85  
; Sequence 85, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Ke  
; APPLICANT: Yang, Shumin  
; APPLICANT: Drelitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 85  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURES:  
; NAME/KEY: CDS  
; LOCATION: (1)..(345)  
US-09-322-409-85  
Alignment Scores:  
Pred. No.: 1,13e-81  
Score: 610.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Query Match: 4  
Gaps: 0  
DB: US-10-787-382-10 (1-115) x US-09-322-409-85 (1-345)

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Db 1 TTGGCTGTAGAAATCCCATGAATAGACTGTGTGCAGAGACCTTGACACAGCTCTCCACT 60  
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsn 40  
Db 61 CATGAACCTGGCTGATAGGCGATGGGAACCTGATGATCTTCTACTCTCTGAAAAATAAAT 120  
Qy 41 HisGlnLeuCyssiIeYsGluValPheGlnGlyIleAspThrLeuYsAsnGlnThrAla 60  
Db 121 CACCACTGTGCATTTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 180  
Qy 61 HisGlyGluAlaValAspYsLeuPheGlnAsnLeuSerLeuIleYsGluHisIleGlu 80  
Db 181 CACGGGAGGCTGTGATTAACCTATTCCTGCTTCTTAATTAAGAACCATAGAG 240  
Qy 81 ArgGlnYsYsArgCyssiIeGlyGluArgTrpArgValThrYsPheLeuAspTrpLeu 100  
Db 241 CGCCAAAAAAGGTGTGCAGGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACTG 300  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 301 CAAGTATTTCTTGGTGTATTAACACGAGTGCACCGGAAAGT 345  
RESULT 2  
US-09-322-409-87/c  
Sequence 87, Application US/09322409  
Patent No. 6471957  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Dretz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C1  
CURRENT APPLICATION NUMBER: US/09/322,409  
CURRENT FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306  
EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 87  
LENGTH: 345  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-09-322-409-87  
Alignment Scores:  
Pred. No.: 1,13e-81 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
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Db 285 CATGAACCTGGCTGATAGGCGATGGGAACCTGATGATCTTCTACTCTCTGAAAAATAAAT 226  
Qy 41 HisGlnLeuCyssiIeYsGluValPheGlnGlyIleAspThrLeuYsAsnGlnThrAla 60  
Db 225 CACCACTGTGCATTTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 166  
Qy 61 HisGlyGluAlaValAspYsLeuPheGlnAsnLeuSerLeuIleYsGluHisIleGlu 80  
Db 61 HisGlyGluAlaValAspYsLeuPheGlnAsnLeuSerLeuIleYsGluHisIleGlu 80

Db 165 CACGGGAGGCTGTGATTAACCTATTCCTTAATTAAGAACCATAGAG 106  
Qy 81 ArgGlnYsYsArgCyssiIeGlyGluArgTrpArgValThrYsPheLeuAspTrpLeu 100  
Db 105 CGCCAAAAAAGGTGTGCAGGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACTG 46  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 45 CAAGTATTTCTTGGTGTATTAACACCGAGTGCACCGGAAAGT 1  
RESULT 3  
US-09-451-527-85  
Sequence 85, Application US/09451527  
Patent No. 6482403  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Dretz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/09/451,527  
CURRENT FILING DATE: 1999-12-01  
EARLIER APPLICATION NUMBER: 09/322,409  
EARLIER FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306  
EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 85  
LENGTH: 345  
TYPE: DNA  
ORGANISM: Canis familiaris  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (1)..(345)  
US-09-451-527-85  
Alignment Scores:  
Pred. No.: 1,13e-81 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
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Db 1 TTTCCTGTAGAAATCCCATGAATAGACTGTGTGCAGAGACCTTGACACAGCTCTCCACT 60  
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsn 40  
Db 61 CATGAACCTGGCTGATAGGCGATGGGAACCTGATGATCTTCTACTCTCTGAAAAATAAAT 120  
Qy 41 HisGlnLeuCyssiIeYsGluValPheGlnGlyIleAspThrLeuYsAsnGlnThrAla 60  
Db 121 CACCACTGTGCATTTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 180  
Qy 61 HisGlyGluAlaValAspYsLeuPheGlnAsnLeuSerLeuIleYsGluHisIleGlu 80  
Db 181 CACGGGAGGCTGTGATTAACCTATTCCTGCTTCTTAATTAAGAACCATAGAG 240  
Qy 81 ArgGlnYsYsArgCyssiIeGlyGluArgTrpArgValThrYsPheLeuAspTrpLeu 100  
Db 241 CGCCAAAAAAGGTGTGCAGGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACTG 300  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 301 CAAGTATTTCTTGGTGTATTAACACCGAGTGCACCGGAAAGT 345

RESULT 4  
US-09-451-527-87/C  
Sequence 87, Application US/09451527  
Patent No. 6482403  
GENERAL INFORMATION:  
APPLICANT: Yang, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Drelitz, Matthew J.  
APPLICANT: Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/09/451,527  
CURRENT FILING DATE: 1999-12-01  
EARLIER APPLICATION NUMBER: 09/322,409  
EARLIER FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306  
EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 87  
LENGTH: 345  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-09-451-527-87  
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DB 285 CATGAACCTGGCGATAGGCGATGGAGAACTGATGATCTTCACTCCGAAATATAAAT 226  
QY 41 HisGlnLeuCySileYsGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
DB 225 CACCAACTGTCATTAAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 166  
QY 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleYsGluHisIleGlu 80  
DB 165 CACGGGAGGCTGTGATTAACCTATCCAAACTGTCTTAATATAAGAACACATAGAG 106  
QY 81 ArgGlnLysLysArgCySAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100  
DB 105 CGCCAAAAAAGAGTGTGCAGAGAAAGATGAGAGACAAAGTTCTTAGACTACTG 46  
QY 101 GlnValPheLeuGlyValIleAsnThrGluThrProGluSer 115  
DB 45 CAAGTATTTCTTGGGTATATAACACGAGTGAACACCGGAAAGT 1  
RESULT 5  
US-09-322-409-83  
Sequence 83, Application US/09322409  
Patent No. 6471957  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Drelitz, Matthew J.  
APPLICANT: Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C1  
CURRENT APPLICATION NUMBER: US/09/322,409  
CURRENT FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306  
EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 84  
LENGTH: 402  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-09-322-409-84  
Alignment Scores:  
Pred. No.: 1,43e-81 Length: 402  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
US-10-787-382-10 (1-115) x US-09-322-409-83 (1-402)

CURRENT FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306  
EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 83  
LENGTH: 402  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-09-322-409-83  
Alignment Scores:  
Pred. No.: 1,43e-81 Length: 402  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
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DB 58 TTTCCTGAGAAATCCCATATAGACTGTGGCAGACCTTGACACTGCTCTCCACT 117  
QY 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40  
DB 118 CATGAACCTGGCGATAGGCGATGGAGAACTGATGATCTTCACTCCGAAATATAAAT 177  
QY 41 HisGlnLeuCySileYsGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
DB 178 CACCAACTGTCATTAAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 237  
QY 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleYsGluHisIleGlu 80  
DB 238 CACGGGAGGCTGTGATTAACCTATCCAAACTGTCTTAATATAAGAACACATAGAG 297  
QY 81 ArgGlnLysLysArgCySAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100  
DB 298 CGCCAAAAAAGAGTGTGCAGAGAAAGATGAGAGACAAAGTTCTTAGACTACTG 357  
QY 101 GlnValPheLeuGlyValIleAsnThrGluThrProGluSer 115  
DB 358 CAAGTATTTCTTGGGTATATAACACGAGTGAACACCGGAAAGT 402  
RESULT 6  
US-09-322-409-84/C  
Sequence 84, Application US/09322409  
Patent No. 6471957  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Drelitz, Matthew J.  
APPLICANT: Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C1  
CURRENT APPLICATION NUMBER: US/09/322,409  
CURRENT FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306  
EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 84  
LENGTH: 402  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-09-322-409-84  
Alignment Scores:  
Pred. No.: 1,43e-81 Length: 402  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-787-382-10 (1-115) x US-09-451-527-83 (1-402)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20  
Db 345 TTTCCTGTAGAAAATCCCATGATAGACTGTGGCAGAGACCTTGACACTGCTCCACT 286

QY 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40  
Db 285 CATGAACCTGGCTGATAGGCGATGGAGAACTGATGATCTTCTACTCTGAAAAATAAAT 226

QY 41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
Db 225 CACCACTGTGCATTTAAAGAACTTTTCAGGGTATAGACATTTGAAGAACCAACCTGCC 166

QY 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80  
Db 165 CACGGGAGGCTGTGATTAACCTATTCCTCAAACTTGCTTAATTAAGAACACATAGAG 106

QY 81 ArgGlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100  
Db 105 CGCCAAAAAAGGTGTGCGAGAGAAAGATGAGAGATGACAAAGTTCTTAGACTACTG 46

QY 101 GlnValPheLeuGlyValIleAsnThrGluTyrThrProGluSer 115  
Db 45 CAAGTATTTCTTGCTGTATTAACACCGAGTGCACCGGAAAGT 1

RESULT 7  
US-09-451-527-83  
Sequence 83, Application US/09451527  
Patent No. 6482403  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kea  
APPLICANT: Yang, Shumin  
APPLICANT: Drelitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/09/451,527  
CURRENT FILING DATE: 1999-12-01  
EARLIER APPLICATION NUMBER: 09/322,409  
EARLIER FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306  
EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 83  
LENGTH: 402  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-09-451-527-83

Alignment Scores:  
Pred. No.: 1,43e-81 Length: 402  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-787-382-10 (1-115) x US-09-451-527-83 (1-402)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20  
Db 58 TTTCCTGTAGAAAATCCCATGATAGACTGTGGCAGAGACCTTGACACTGCTCCACT 117

QY 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40  
Db 118 CATGAACCTGGCTGATAGGCGATGGAGAACTGATGATCTTACTCTGAAAAATTAAT 177

QY 41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
Db 178 CACCACTGTGCATTTAAAGAACTTTTCAGGGTATAGACATTTGAAGAACCAACCTGCC 237

QY 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80  
Db 238 CACGGGAGGCTGTGATTAACCTATTCCTCAAACTTGCTTAATTAAGAACACATAGAG 297

QY 81 ArgGlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100  
Db 298 CGCCAAAAAAGGTGTGCGAGAGAAAGATGAGAGATGACAAAGTTCTTAGACTACTG 357

QY 101 GlnValPheLeuGlyValIleAsnThrGluTyrThrProGluSer 115  
Db 358 CAAGTATTTCTTGCTGTATTAACACCGAGTGCACCGGAAAGT 402

RESULT 8  
US-09-451-527-84/c  
Sequence 84, Application US/09451527  
Patent No. 6482403  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kea  
APPLICANT: Yang, Shumin  
APPLICANT: Drelitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/09/451,527  
CURRENT FILING DATE: 1999-12-01  
EARLIER APPLICATION NUMBER: 09/322,409  
EARLIER FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306  
EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 84  
LENGTH: 402  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-09-451-527-84

Alignment Scores:  
Pred. No.: 1,43e-81 Length: 402  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-787-382-10 (1-115) x US-09-451-527-84 (1-402)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20  
Db 345 TTTCCTGTAGAAAATCCCATGATAGACTGTGGCAGAGACCTTGACACTGCTCCACT 286

QY 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40  
Db 285 CATGAACCTGGCTGATAGGCGATGGAGAACTGATGATCTTCTACTCTGAAAAATAAAT 226

QY 41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
Db 225 CACCACTGTGCATTTAAAGAACTTTTCAGGGTATAGACATTTGAAGAACCAACCTGCC 166

QY 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80  
Db 165 CACGGGAGGCTGTGATTAACCTATTCCTCAAACTTGCTTAATTAAGAACACATAGAG 106

QY 81 ArgGlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100  
Db 105 CGCCAAAAAAGGTGTGCGAGAGAAAGATGAGAGATGACAAAGTTCTTAGACTACTG 46



Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 45 CAAGTATTTCTTGGTGTATTAACACCGAGTGCACCGGAAAGT 1

RESULT 9  
US-09-322-409-80  
; Sequence 80, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Drelitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29)..(430)  
US-09-322-409-80

Alignment Scores:  
Pred. No.: 2,71e-81 Length: 610  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-787-382-10 (1-115) x US-09-322-409-80 (1-610)

Qy 1 PheAlaValGluAnPProMetAsnArgLeuValAlaGluTrpThrLeuLeuSerThr 20  
Db 86 TTTCTGTAGAAATCCCATGATGACTGTGGCAGAGACTTGACACTCTCTCCACT 145

Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40  
Db 146 CATGGAAGTGGCTGATGAGCGGATGGGAACTGATGATTCCTACTCCTGAAATTAAT 205

Qy 41 HisGlnLeuCySilelysgluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
Db 206 CACCAACTGTCATTAAAGAGTTTTCAGGGTATAGACATTTGAAAGAACCAACTGCC 265

Qy 61 HisGlyGluAlaValAspLeuPheGlnAsnLeuSerLeuIlelysgluHisIleGlu 80  
Db 266 CACGGGAGGCTGTGATTAACCTATTCCTGCTTTTAAATTAAGAACCACTGAG 325

Qy 81 ArgGlnLysLysArgCySAlaGlyLysArgTrpArgValThrLysPheLeuAspTyrLeu 100  
Db 326 CGCCAAAAAAGAGTGTGACAGAGAAAGATGAGAGTGAACAAGTTCTTACTGACTG 385

Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 386 CAAGTATTTCTTGGTGTATTAACACCGAGTGCACCGGAAAGT 430

RESULT 10  
US-09-322-409-82/c  
; Sequence 82, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Drelitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 82  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-322-409-82

Alignment Scores:  
Pred. No.: 2,71e-81 Length: 610  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-787-382-10 (1-115) x US-09-322-409-82 (1-610)

Qy 1 PheAlaValGluAnPProMetAsnArgLeuValAlaGluTrpThrLeuLeuSerThr 20  
Db 525 TTTCTGTAGAAATCCCATGATGACTGTGGCAGAGACTTGACACTCTCTCCACT 466

Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40  
Db 465 CATGGAAGTGGCTGATGAGCGGATGGGAACTGATGATTCCTACTCCTGAAATTAAT 406

Qy 41 HisGlnLeuCySilelysgluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
Db 405 CACCAACTGTCATTAAAGAGTTTTCAGGGTATAGACATTTGAAAGAACCAACTGCC 346

Qy 61 HisGlyGluAlaValAspLeuPheGlnAsnLeuSerLeuIlelysgluHisIleGlu 80  
Db 345 CACGGGAGGCTGTGATTAACCTATTCCTGCTTTTAAATTAAGAACCACTGAG 286

Qy 81 ArgGlnLysLysArgCySAlaGlyLysArgTrpArgValThrLysPheLeuAspTyrLeu 100  
Db 285 CGCCAAAAAAGAGTGTGACAGAGAAAGATGAGAGTGAACAAGTTCTTACTGACTG 226

Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 225 CAAGTATTTCTTGGTGTATTAACACCGAGTGCACCGGAAAGT 181

RESULT 11  
US-09-451-527-80  
; Sequence 80, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Drelitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 610  
; TYPE: DNA

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; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-451-527-80

Alignment Scores:
Pred. No.: 2,71e-81      Length: 610
Score: 610.00           Matches: 115
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 4                   Gaps: 0

US-10-787-382-10 (1-115) x US-09-451-527-80 (1-610)
Qy 1 PheAlaValGluAenPromeCAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
Db 86 TTTCCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACT 145
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
Db 146 CATGAACCTGGCTGATAGGCGATGGAGACCTGATGATTCCTACTCTCGAAAATATAAAT 205
Qy 41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60
Db 206 CACCAACTGTGCATTTAAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCC 265
Qy 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
Db 266 CACGGGAGGCTGTGGATTAACCTATTCCTGTTTAAATAAAGAACACATAGAG 325
Qy 81 ArgGlnLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100
Db 326 CGCCAAAAAAGAGTGTGCAGAGAAAGATGAGAGGACAAAGTTCTGACTTACTG 385
Qy 101 GlnValPheLeuGlyValIleAsnThrGluThrProGluSer 115
Db 386 CAAGTATTTCTGTGTATTAACACCGAGTGACACCGGAAAGT 430

RESULT 12
US-09-451-527-82/c
; Sequence 82, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-82

Alignment Scores:
Pred. No.: 2,71e-81      Length: 610
Score: 610.00           Matches: 115
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 4                   Gaps: 0
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US-10-787-382-10 (1-115) x US-09-451-527-82 (1-610)
Qy 1 PheAlaValGluAenPromeCAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
Db 525 TTTCCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACT 466
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
Db 465 CATGAACCTGGCTGATAGGCGATGGAGACCTGATGATTCCTACTCTCGAAAATATAAAT 406
Qy 41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60
Db 405 CACCAACTGTGCATTTAAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCC 346
Qy 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
Db 345 CACGGGAGGCTGTGGATTAACCTATTCCTGTTTAAATAAAGAACACATAGAG 286
Qy 81 ArgGlnLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100
Db 285 CGCCAAAAAAGAGTGTGCAGAGAAAGATGAGAGTGAACAAAGTTCTTGAAGACTACTG 226
Qy 101 GlnValPheLeuGlyValIleAsnThrGluThrProGluSer 115
Db 225 CAAGTATTTCTGTGTATTAACACCGAGTGACACCGGAAAGT 181

RESULT 13
US-09-371-615A-1
; Sequence 1, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; FILE REFERENCE: 03604001700US00
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-371-615A-1

Alignment Scores:
Pred. No.: 3,19e-80      Length: 405
Score: 601.00           Matches: 114
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 1
Query Match: 98.52%      Indels: 0
DB: 4                   Gaps: 0

US-10-787-382-10 (1-115) x US-09-371-615A-1 (1-405)
Qy 1 PheAlaValGluAenPromeCAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
Db 58 TTTCCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACT 117
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
Db 118 CATGAACCTGGCTGATAGGCGATGGAGACCTGATGATTCCTACTCTCGAAAATATAAAT 177
Qy 41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60
Db 178 CACCAACTGTGCATTTAAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCC 237
Qy 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
Db 238 CACGGGAGGCTGTGGATTAACCTATTCCTGTTTAAATAAAGAACACATAGAG 297
Qy 81 ArgGlnLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100
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Db 298 CGCCAAAAAAGGTGGAGGAGAAAGATGAGAGCAAAAGTCTGAGCACTG 357  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 358 CAAGTATTTCTTGGTGTATATAACCCAGATGACCAATGAAAGT 402

## RESULT 14

US-09-839-2  
; Sequence 2, Application US/09079839  
; Patent No. 6048726  
; GENERAL INFORMATION:  
; APPLICANT: Welleman, Joel K.  
; APPLICANT: Karim, Afrah S.  
; TITLE OF INVENTION: INHIBITION OF EOSINOPHILIC INFLAMMATION  
; FILE REFERENCE: 09998/002001  
; CURRENT APPLICATION NUMBER: US/09/079, 839  
; CURRENT FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 816  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-839-2

Alignment Scores:  
Pred. No.: 3,64e-43 Length: 816  
Score: 356.00 Matches: 70  
Percent Similarity: 76.79% Conservative: 16  
Best Local Similarity: 62.50% Mismatches: 26  
Query Match: 58.36% Indels: 0  
DB: 3 Gaps: 0

US-10-787-382-10 (1-115) x US-09-079-839-2 (1-816)

Qy 4 GluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHisArgThr 23  
Db 111 GAAATTCACACAGTGCATTGGTGAAGACCTTGGACATGCTTTCTACTCATCGAACT 170  
Qy 24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43  
Db 171 CTGCTGATAGCCAAATGAGACTCTGAGATTCCTGCTGCTGACATAAAATCAACCAATG 230  
Qy 44 CysIleLeuGlyValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHisGlyGlu 63  
Db 231 TGCACGTGAAGAACTTTCAAGGAAATAGCACACTGAGAGTCAAACTGTCCAAGGGGT 290  
Qy 64 AlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGlnHisIleGluArgGlnLys 83  
Db 291 ACTGTGAAGACATTAATCAAAACTGTCTTAATAAAGAAATACATTGACGGCCAAA 350  
Qy 84 LysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGlnValPhe 103  
Db 351 AAAAAGTGTGAGAAAGAAAGCGAGATAACCAATTCCTAGACTACCTCAAGAGTTT 410  
Qy 104 LeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 411 CTGTGTATATGAACACCGAGTGTATATAGAAAGT 446

## RESULT 15

US-09-180-864-1  
; Sequence 1, Application US/09180864  
; Patent No. 6465616  
; GENERAL INFORMATION:  
; APPLICANT: Lopez, Angel  
; APPLICANT: Vadas, Matthew  
; APPLICANT: Shannon, Frances  
; APPLICANT: Baetiras, Stan  
; APPLICANT: Hey, Allan W  
; TITLE OF INVENTION: AN INTERLEUKIN-5 ANTAGONIST  
; FILE REFERENCE: 99722  
; CURRENT APPLICATION NUMBER: US/09/180, 864

; CURRENT FILING DATE: 1999-04-12  
; PRIOR APPLICATION NUMBER: 08/591,438  
; PRIOR FILING DATE: 1994-07-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 377  
; TYPE: DNA  
; ORGANISM: nucleotide sequence encoding modified IL-5  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (4)...(366)  
US-09-180-864-1

Alignment Scores:  
Pred. No.: 6,22e-43 Length: 377  
Score: 351.00 Matches: 69  
Percent Similarity: 75.89% Conservative: 16  
Best Local Similarity: 61.61% Mismatches: 27  
Query Match: 57.54% Indels: 0  
DB: 3 Gaps: 0

US-10-787-382-10 (1-115) x US-09-180-864-1 (1-377)

Qy 4 GluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHisArgThr 23  
Db 31 GAAATTCACACAGTGCATTGGTGAAGACCTTGGACATGCTTTCTACTCATCGAACT 90  
Qy 24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43  
Db 91 CTGCTGATAGCCAAATGAGACTCTGAGATTCCTGCTGCTGACATAAAATCAACCAATG 150  
Qy 44 CysIleLeuGlyValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHisGlyGlu 63  
Db 151 TGCACGTGAAGAACTTTCAAGGAAATAGCACACTGAGAGTCAAACTGTCCAAGGGGT 210  
Qy 64 AlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGlnHisIleGluArgGlnLys 83  
Db 211 ACTGTGAAGACATTAATCAAAACTGTCTTAATAAAGAAATACATTGACGGCCAAAG 270  
Qy 84 LysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGlnValPhe 103  
Db 271 AAAAAGTGTGAGAAAGAAAGCGAGATAACCAATTCCTGAGACTACCTCAAGAGTTT 330  
Qy 104 LeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 331 CTGTGTATATGAACACCGAGTGTATATAGAAAGT 366

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Job time : 104.068 secs

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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 6, 2005, 22:43:11 ; Search time 477.55 Seconds

(without alignments)  
1561.024 Million cell updates/sec

Title: US-10-787-382-10

Perfect score: 610  
Sequence: 1 PAYENPMNRVLAETITLIST.....FLDYLYQVFLGVINTEWTPES 115

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 7297361 seqs, 324162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -OPMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPC=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -WATTS-blosum62  
-TRANS=human40.cdd -LIST=45 -DOCNALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US10787382@cgn 1.1.879 @runat\_04082005\_084754\_19405  
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Published Applications NA.\*  
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4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/PCFUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/2/pubpna/US10I\_NEW\_PUB.seq.\*  
23: /cgn2\_6/ptodata/2/pubpna/US11\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	610	100.0	345	9 US-09-755-633-9	Sequence 9, Appli
2	610	100.0	345	9 US-09-755-633-11	Sequence 11, Appli
3	610	100.0	345	14 US-10-218-654-85	Sequence 8, Appli
4	610	100.0	345	14 US-10-218-654-87	Sequence 87, Appli
5	610	100.0	345	15 US-10-262-439-85	Sequence 85, Appli
6	610	100.0	345	15 US-10-262-439-87	Sequence 87, Appli
7	610	100.0	345	19 US-10-787-382-9	Sequence 9, Appli
8	610	100.0	345	19 US-10-787-382-11	Sequence 11, Appli
9	610	100.0	402	9 US-09-755-633-7	Sequence 7, Appli
10	610	100.0	402	9 US-09-755-633-8	Sequence 8, Appli
11	610	100.0	402	14 US-10-218-654-83	Sequence 83, Appli
12	610	100.0	402	14 US-10-218-654-84	Sequence 84, Appli
13	610	100.0	402	15 US-10-262-439-83	Sequence 83, Appli
14	610	100.0	402	15 US-10-262-439-84	Sequence 84, Appli
15	610	100.0	402	19 US-10-787-382-7	Sequence 7, Appli
16	610	100.0	402	19 US-10-787-382-8	Sequence 8, Appli
17	610	100.0	610	9 US-09-755-633-6	Sequence 6, Appli
18	610	100.0	610	14 US-10-218-654-80	Sequence 80, Appli
19	610	100.0	610	14 US-10-218-654-82	Sequence 82, Appli
20	610	100.0	610	15 US-10-262-439-80	Sequence 80, Appli
21	610	100.0	610	15 US-10-262-439-82	Sequence 82, Appli
22	610	100.0	610	19 US-10-787-382-4	Sequence 4, Appli
23	610	100.0	610	19 US-10-787-382-6	Sequence 6, Appli
24	610	100.0	610	9 US-09-755-633-21	Sequence 21, Appli
25	546.5	89.6	671	9 US-10-787-382-21	Sequence 21, Appli
26	546.5	89.6	671	19 US-10-787-382-21	Sequence 19, Appli
27	363	59.5	1658	9 US-09-755-633-19	Sequence 19, Appli
28	363	59.5	1658	19 US-10-787-382-19	Sequence 19, Appli
29	363	59.5	1658	9 US-09-755-633-18	Sequence 18, Appli
30	363	59.5	1658	19 US-10-787-382-18	Sequence 18, Appli
31	357	58.5	864	16 US-10-295-074-12	Sequence 12, Appli
32	357	58.5	864	20 US-10-846-911-12	Sequence 12, Appli
33	356	58.4	459	22 US-10-880-101A-85	Sequence 85, Appli
34	356	58.4	816	17 US-10-191-997-90	Sequence 90, Appli
35	356	58.4	816	21 US-10-929-182-4	Sequence 4, Appli
36	356	58.4	816	22 US-10-880-101A-87	Sequence 87, Appli
37	356	58.4	858	16 US-10-295-074-8	Sequence 8, Appli
38	356	58.4	858	16 US-10-295-074-10	Sequence 10, Appli
39	356	58.4	858	20 US-10-846-911-8	Sequence 8, Appli
40	356	58.4	858	20 US-10-846-911-10	Sequence 10, Appli
41	356	58.4	864	16 US-10-295-074-14	Sequence 14, Appli
42	356	58.4	864	20 US-10-846-911-14	Sequence 14, Appli
43	350	57.4	816	18 US-10-641-643-1236	Sequence 1236, Ap
44	228.5	37.5	3241	22 US-10-880-101A-91	Sequence 91, Appli
45	222	36.4	6727	9 US-09-800-629A-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-09-755-633-9  
; Sequence 9, Application US/09755633  
; Patent No. US20020127200A1  
GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-CI-CI  
; CURRENT APPLICATION NUMBER: US/09/755, 633  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306

Pred. No. is the number of results predicted by chance to have a

/ PRIOR FILING DATE: 1998-05-29  
/ NUMBER OF SEQ ID NOS: 21  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 9  
/ LENGTH: 345  
/ TYPE: DNA  
/ ORGANISM: Canis familiaris  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: (1)..(345)  
US-09-755-633-9

Alignment Scores:  
Pred. No.: 4,78e-78 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-787-382-10 (1-115) x US-09-755-633-9 (1-345)

Qy 1 PheAlaValGluAenProMetAenArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 1 TTGCTGTAGAAATCCCATGAATAGACTGTGGCAGAGACTTGACACTGCTCTCACT 60  
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAenIleAsn 40  
Db 61 CATGAACTTGCTGTAGAGGAGTGGAACTGATGATCTTACTCTGAAAAATAAAAAT 120  
Qy 41 HisGlnLeuCySileysGluValPheGlnGlyIleAspThrLeuIleAsnGlnThrAla 60  
Db 121 CACCACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACATTAAGAAACCAAACTGCC 180  
Qy 61 HisGlyValGluAenProMetAenArgLeuValAlaGluThrLeuThrLeuLeuSerThr 80  
Db 181 CACGGAGAGCTGTGATTAACCTATTCCTCAAACTTGCTTAAATAAAGAACATAGAG 240  
Qy 81 ArgGlnIleYsArgCySalaGlyGluArgTrpArgValThrIysPheLeuAspTyrLeu 100  
Db 241 CGCCAAAAAAGAGTGTGCAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 301 CAAGTATTCTTGCTGTATTAACCAAGAGTGCACCGGAAAGT 345

## RESULT 2

US-09-755-633-11/C  
/ Sequence 11, Application US/09755633  
/ Patent No. US20020127200A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Yang, Shumin  
/ APPLICANT: Weber, Eric R.  
/ APPLICANT: McCall, Catherine A.  
/ TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
/ FILE REFERENCE: IM-2-C1-C1  
/ CURRENT APPLICATION NUMBER: US/09/755,633  
/ PRIOR FILING DATE: 2001-01-05  
/ PRIOR APPLICATION NUMBER: 09/322,409  
/ PRIOR FILING DATE: 1999-05-28  
/ PRIOR APPLICATION NUMBER: 60/087,306  
/ NUMBER OF SEQ ID NOS: 21  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 11  
/ LENGTH: 345  
/ TYPE: DNA  
/ ORGANISM: Canis familiaris  
US-09-755-633-11

Alignment Scores: 4,78e-78 Length: 345  
Pred. No.: 4,78e-78 Length: 345

Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-787-382-10 (1-115) x US-09-755-633-11 (1-345)

Qy 1 PheAlaValGluAenProMetAenArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 345 TTGCTGTAGAAATCCCATGAATAGACTGTGGCAGAGACTTGACACTGCTCTCACT 286  
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAenIleAsn 40  
Db 285 CATGAACTTGCTGTAGAGGAGTGGAACTGATGATCTTACTCTGAAAAATAAAAAT 226  
Qy 41 HisGlnLeuCySileysGluValPheGlnGlyIleAspThrLeuIleAsnGlnThrAla 60  
Db 225 CACCACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACATTAAGAAACCAAACTGCC 166  
Qy 61 HisGlyValGluAenProMetAenArgLeuValAlaGluThrLeuThrLeuLeuSerThr 80  
Db 165 CACGGAGAGCTGTGATTAACCTATTCCTCAAACTTGCTTAAATAAAGAACATAGAG 106  
Qy 81 ArgGlnIleYsArgCySalaGlyGluArgTrpArgValThrIysPheLeuAspTyrLeu 100  
Db 105 CGCCAAAAAAGAGTGTGCAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 46  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 45 CAAGTATTCTTGCTGTATTAACCAAGAGTGCACCGGAAAGT 1

## RESULT 3

US-10-218-654-85  
/ Sequence 85, Application US/10218654  
/ Publication No. US2003009603A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Sim, Gek-Kee  
/ APPLICANT: Yang, Shumin  
/ APPLICANT: Dreitz, Matthew J.  
/ APPLICANT: Mondeling, Ramon S.  
/ TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
/ FILE REFERENCE: IM-2-C1  
/ CURRENT APPLICATION NUMBER: US/10/218,654  
/ PRIOR FILING DATE: 2002-08-13  
/ PRIOR APPLICATION NUMBER: US/09/322,409  
/ PRIOR FILING DATE: 1999-05-28  
/ PRIOR APPLICATION NUMBER: 60/087,306  
/ NUMBER OF SEQ ID NOS: 154  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 85  
/ LENGTH: 345  
/ TYPE: DNA  
/ ORGANISM: Canis familiaris  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: (1)..(345)  
US-10-218-654-85

Alignment Scores:  
Pred. No.: 4,78e-78 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-787-382-10 (1-115) x US-10-218-654-85 (1-345)

Qy 1 PheAlaValGluAenProMetAenArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 1 TTGCTGTAGAAATCCCATGAATAGACTGTGGCAGAGACTTGACACTGCTCTCACT 60

Db 1 TTTCGTGAGAAATCCCATGATAGACTGGTGAGACCTTGACACTGCTCCACT 60  
Qy 21 HIsArGhTrTpLeuIlleGlyAspGlyAsnLeuWetIleProThrProGluAsnLyAsn 40  
Db 61 CATGAACCTGGCTGATAGAGGAGATGGAACTGATGATCTTCTACTCCCTGAAAAATAAAT 120  
Qy 41 HIsGlnLeuCySileYsGluValPheGlnGlyIleAspThrLeuLyAsnGlnThrAla 60  
Db 121 CACCAACTGTCATTAAAGAACTTTTTCAGGGATATAGACATTGAGAACCAACTGCC 180  
Qy 61 HIsGlyGluAlaValAspLyLeuPheGlnAsnLeuSerLeuIleYsGluHisIleGlu 80  
Db 181 CACGGGAGGCTGTGATTAACCTATTCAAAACCTTGTCTTTAATTAAGAACACATGAG 240  
Qy 81 ArgGlnLyLeuYsArgCySAlaGlyGluArgTrpArgValThrLyPheLeuAspTyrLeu 100  
Db 241 CGCCAAAAAAGAGTGTGACGAGAAAGATGAGAGAGAACAAAGTTCTTACTGACTACTG 300  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 301 CAAGTATTTCTTGGTGTATTAACACCGAGTGCACCGGAAAGT 345

## RESULT 4

US-10-218-654-87/c  
; Sequence 87, Application US/10218654  
; Publication No. US2003009609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218, 654  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 87  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-218-654-87

## Alignment Scores:

Pred. No.: 4,78e-78 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-787-382-10 (1-115) x US-10-218-654-87 (1-345)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 345 TTTCGTGAGAAATCCCATGATAGACTGGTGACAGAACTTGACACTGCTCCACT 286  
Qy 21 HIsArGhTrTpLeuIlleGlyAspGlyAsnLeuWetIleProThrProGluAsnLyAsn 40  
Db 285 CATGAACCTGGCTGATAGAGGAGATGGAACTGATGATCTTCTACTCCCTGAAAAATAAAT 226  
Qy 41 HIsGlnLeuCySileYsGluValPheGlnGlyIleAspThrLeuLyAsnGlnThrAla 60  
Db 225 CACCAACTGTCATTAAAGAACTTTTTCAGGGATATAGACATTGAGAACCAACTGCC 166  
Qy 61 HIsGlyGluAlaValAspLyLeuPheGlnAsnLeuSerLeuIleYsGluHisIleGlu 80  
Db 165 CACGGGAGGCTGTGATTAACCTATTCAAAACCTTGTCTTTAATTAAGAACACATGAG 106

Qy 81 ArgGlnLyLeuYsArgCySAlaGlyGluArgTrpArgValThrLyPheLeuAspTyrLeu 100  
Db 105 CGCCAAAAAAGAGTGTGACGAGAAAGATGAGAGAGAACAAAGTTCTTACTGACTACTG 46  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 45 CAAGTATTTCTTGGTGTATTAACACCGAGTGCACCGGAAAGT 1

## RESULT 5

US-10-262-439-85  
; Sequence 85, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 85  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; NAME/KEY: CDS  
; LOCATION: (1)..(345)  
US-10-262-439-85

## Alignment Scores:

Pred. No.: 4,78e-78 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 15 Gaps: 0

US-10-787-382-10 (1-115) x US-10-262-439-85 (1-345)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 1 TTTCGTGAGAAATCCCATGATAGACTGGTGACAGAACTTGACACTGCTCCACT 60  
Qy 21 HIsArGhTrTpLeuIlleGlyAspGlyAsnLeuWetIleProThrProGluAsnLyAsn 40  
Db 61 CATGAACCTGGCTGATAGAGGAGATGGAACTGATGATCTTCTACTCCCTGAAAAATAAAT 120  
Qy 41 HIsGlnLeuCySileYsGluValPheGlnGlyIleAspThrLeuLyAsnGlnThrAla 60  
Db 121 CACCAACTGTCATTAAAGAACTTTTTCAGGGATATAGACATTGAGAACCAACTGCC 180  
Qy 61 HIsGlyGluAlaValAspLyLeuPheGlnAsnLeuSerLeuIleYsGluHisIleGlu 80  
Db 181 CACGGGAGGCTGTGATTAACCTATTCAAAACCTTGTCTTTAATTAAGAACACATGAG 240  
Qy 81 ArgGlnLyLeuYsArgCySAlaGlyGluArgTrpArgValThrLyPheLeuAspTyrLeu 100  
Db 241 CGCCAAAAAAGAGTGTGACGAGAAAGATGAGAGAGAACAAAGTTCTTACTGACTACTG 300  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 301 CAAGTATTTCTTGGTGTATTAACACCGAGTGCACCGGAAAGT 345

RESULT 6  
US-10-262-439-87/c  
Sequence 87, Application US/10262439  
Publication No. US20030143196A1  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Dreitz, Matthew J.  
APPLICANT: Mondeling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/10/262,439  
CURRENT FILING DATE: 2002-09-30  
PRIOR APPLICATION NUMBER: US/09/451,527  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 87  
LENGTH: 345  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-10-262-439-87

Alignment Scores:  
Pred. No.: 4,78e-78 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-787-382-10 (1-115) x US-10-262-439-87 (1-345)

Qy 1 PheAlaValGluAnpPromeTaanArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 345 TTTCTGTAGAAATCCCATATAATAGACTGTGGCAGAGACTTGACCTGCTCCACT 286  
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleAsn 40  
Db 285 CATGAACCTTGCTGATAGCGGATGGGAACTGATGATCTTACTCTGAAAAATAAAAAT 226  
Qy 41 HisGlnLeuCySilelyGluValPheGlnGlyIleAspThrLeuIleAsnGlnThrAla 60  
Db 225 CACCACTGTGCAATTAAAGAAAGTTTTCAGGGTATAGACATTTGAAAGAACCAACTGCC 166  
Qy 61 HisGlyGluAlaValAspIleuPheGlnAsnLeuSerLeuIlelyGluHisIleGlu 80  
Db 165 CACGGAGGCTGTGGATTAACATATCCAAACTTGTCTTTAATTAAGAACACATAGAG 106  
Qy 81 ArgGlnIleuIleAspIleGlyValGluArgTrpArgValThrIlePheLeuAspIleu 100  
Db 105 CGCCAAAAAAGGTGTGCGAGGAAAGATGGAAGTGAACAAAGTTCTTAGACTACTG 46  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 45 CAAGTATTTCTTGTGTATTAACACCGAGTGGACCGGAAAGT 1  
RESULT 7  
US-10-787-382-9  
Sequence 9, Application US/10787382  
Publication No. US20040191868A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Shumin  
APPLICANT: McCall, Catherine A.  
APPLICANT: Weber, Eric R.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
ACID MOLECULES, AND USES THEREOF

FILE REFERENCE: IM-2-C1-C1  
CURRENT APPLICATION NUMBER: US/10/787,382  
CURRENT FILING DATE: 2004-02-24  
PRIOR APPLICATION NUMBER: US/09/755,633  
PRIOR FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 345  
TYPE: DNA  
ORGANISM: Canis familiaris  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1..(345))  
US-10-787-382-9

Alignment Scores:  
Pred. No.: 4,78e-78 Length: 345  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-787-382-10 (1-115) x US-10-787-382-9 (1-345)

Qy 1 PheAlaValGluAnpPromeTaanArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 1 TTTCTGTAGAAATCCCATATAATAGACTGTGGCAGAGACTTGACCTGCTCCACT 60  
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleAsn 40  
Db 61 CATGAACCTTGCTGATAGCGGATGGGAACTGATGATCTTACTCTGAAAAATAAAAAT 120  
Qy 41 HisGlnLeuCySilelyGluValPheGlnGlyIleAspThrLeuIleAsnGlnThrAla 60  
Db 121 CACCACTGTGCAATTAAAGAAAGTTTTCAGGGTATAGACATTTGAAAGAACCAACTGCC 180  
Qy 61 HisGlyGluAlaValAspIleuPheGlnAsnLeuSerLeuIlelyGluHisIleGlu 80  
Db 181 CACGGAGGCTGTGGATTAACATATCCAAACTTGTCTTTAATTAAGAACACATAGAG 240  
Qy 81 ArgGlnIleuIleAspIleGlyValGluArgTrpArgValThrIlePheLeuAspIleu 100  
Db 241 CGCCAAAAAAGGTGTGCGAGGAAAGATGGAAGTGAACAAAGTTCTTAGACTACTG 300  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115  
Db 301 CAAGTATTTCTTGTGTATTAACACCGAGTGGACCGGAAAGT 345  
RESULT 8  
US-10-787-382-11/c  
Sequence 11, Application US/10787382  
Publication No. US20040191868A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Shumin  
APPLICANT: McCall, Catherine A.  
APPLICANT: Weber, Eric R.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C1-C1  
CURRENT APPLICATION NUMBER: US/10/787,382  
CURRENT FILING DATE: 2004-02-24  
PRIOR APPLICATION NUMBER: US/09/755,633  
PRIOR FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 306  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 345  
TYPE: DNA  
ORGANISM: Canis familiaris  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1..(345))  
US-10-787-382-11





Db 225 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACATTGAAGAACCAACTGCC 166  
Qy HisGlyGluAlaValAspLeuPheGlnAsnLeuSerLeuIleuYsgLuhIleGlu 80  
Db 165 CACGGGAGGCTGTGATTAACCTATTCCTCAAACTGTCTTTAATAAAGAACACATAGAG 106  
Qy ArgGlnIlyAsnArgCyAlaGlyGluArgTTPArgValThirLysPheLeuAspTyrLeu 100  
Db 105 CGCCAAAATAAAGGTGTGCAGAGAAAGATGAGAGTGAACAAAGTTCCTAGACTACTG 46  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTTPThrProGluSer 115  
Db 45 CAAGTATTTCTTGTGTATTAACACCGAGTGAACCGGAAAGT 1

## RESULT 11

US-10-218-654-83  
Sequence 83, Application US/10218654  
Publication No. US2003009609A1  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Ke  
APPLICANT: Yang, Shumin  
APPLICANT: Drelitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C1  
CURRENT APPLICATION NUMBER: US/10/218,654  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: US/09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 83  
LENGTH: 402  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-10-218-654-83

## Alignment Scores:

Pred. No.: 5,99e-78 Length: 402  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-787-382-10 (1-115) x US-10-218-654-83 (1-402)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 58 TTTCGTGTAGAAATCCCATATTAAGACTGTGCGACAGACTTGACACTGCTCTCCACT 117  
Qy 21 HisArgThrTTPLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40  
Db 118 CATGAACCTTGCTGATGCGATGCGATGGAACTGATGATTCCTACTCCGAAAATAAAAT 177  
Qy 41 HisGlnLeuCyAlaIlyAsnGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
Db 178 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACTTGAAGAACCAAACTGCC 237  
Qy 61 HisGlyGluAlaValAspLeuPheGlnAsnLeuSerLeuIleuYsgLuhIleGlu 80  
Db 238 CACGGGAGGCTGTGATTAACCTATTCCTCAAACTGTCTTTAATAAAGAACACATAGAG 297  
Qy 81 ArgGlnIlyAsnArgCyAlaGlyGluArgTTPArgValThirLysPheLeuAspTyrLeu 100  
Db 298 CGCCAAAATAAAGGTGTGCAGAGAAAGATGAGAGTGAACAAAGTTCCTAGACTACTG 357  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTTPThrProGluSer 115  
Db 358 CAAGTATTTCTTGTGTATTAACACCGAGTGAACCGGAAAGT 402

## RESULT 12

US-10-218-654-84/C  
Sequence 84, Application US/10218654  
Publication No. US2003009609A1  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Ke  
APPLICANT: Yang, Shumin  
APPLICANT: Drelitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C1  
CURRENT APPLICATION NUMBER: US/10/218,654  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: US/09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 84  
LENGTH: 402  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-10-218-654-84

## Alignment Scores:

Pred. No.: 5,99e-78 Length: 402  
Score: 610.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-787-382-10 (1-115) x US-10-218-654-84 (1-402)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20  
Db 345 TTTCGTGTAGAAATCCCATATTAAGACTGTGCGACAGACTTGACACTGCTCTCCACT 286  
Qy 21 HisArgThrTTPLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40  
Db 285 CATGAACCTTGCTGATGCGATGCGATGGAACTGATGATTCCTACTCCGAAAATAAAAT 226  
Qy 41 HisGlnLeuCyAlaIlyAsnGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60  
Db 225 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACTTGAAGAACCAAACTGCC 166  
Qy 61 HisGlyGluAlaValAspLeuPheGlnAsnLeuSerLeuIleuYsgLuhIleGlu 80  
Db 165 CACGGGAGGCTGTGATTAACCTATTCCTCAAACTGTCTTTAATAAAGAACACATAGAG 106  
Qy 81 ArgGlnIlyAsnArgCyAlaGlyGluArgTTPArgValThirLysPheLeuAspTyrLeu 100  
Db 105 CGCCAAAATAAAGGTGTGCAGAGAAAGATGAGAGTGAACAAAGTTCCTAGACTACTG 46  
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTTPThrProGluSer 115  
Db 45 CAAGTATTTCTTGTGTATTAACACCGAGTGAACCGGAAAGT 1

RESULT 13  
US-10-262-439-83  
Sequence 83, Application US/10262439  
Publication No. US20030143196A1  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Ke  
APPLICANT: Yang, Shumin  
APPLICANT: Drelitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C2

```

; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-83

Alignment Scores:
Pred. No.: 5,99e-78 Length: 402
Score: 610.00 Matches: 115
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-787-382-10 (1-115) x US-10-262-439-83 (1-402)

Qy 1 PheAlaValGluAenProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
Db 58 TTTCTGTAGAAAATCCCATGAATAGACTGTGCAGAGACCTTGACACTGCTCCCACT 117
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
Db 118 CATGAACTTGCTGATAGCGATGGCACTGATGATCTTCTCTGAAAATTAAT 177
Qy 41 HisGlnLeuCybIleYsGluValPheGlnGlyIleAspThrLeuYsAsnGlnThrAla 60
Db 178 CACCAACTGTCATTAAGAAGTTTTCAGGGTATAGACATGGAACCAACTGCC 237
Qy 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleYsGluHisIleGlu 80
Db 238 CACGGGGAGCTGTGGATTAACCTATCCAAACTTGTCTTAATTAAGAACACATAGAG 297
Qy 81 ArgGlnLysLysArgCybAlaGlyGluArgTrpArgValThrLysPheLeuAspTrpLeu 100
Db 298 GCCCAAAAAAAGGTGTGCAGAGAAAGATGAGAGTGAACAAGTTCTTACTACTG 357
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
Db 358 CAAGTATTCTTGGTGTATTAACCGAGTGGACACCGGAAAGT 402

RESULT 14
US-10-262-439-84/c
; Sequence 84, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kea
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84
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; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-84

Alignment Scores:
Pred. No.: 5,99e-78 Length: 402
Score: 610.00 Matches: 115
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-787-382-10 (1-115) x US-10-262-439-84 (1-402)

Qy 1 PheAlaValGluAenProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
Db 345 TTTCTGTAGAAAATCCCATGAATAGACTGTGCAGAGACCTTGACACTGCTCCCACT 286
Qy 21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
Db 285 CATGAACTTGCTGATAGCGATGGCACTGATGATCTTCTCTGAAAATTAAT 226
Qy 41 HisGlnLeuCybIleYsGluValPheGlnGlyIleAspThrLeuYsAsnGlnThrAla 60
Db 225 CACCAACTGTCATTAAGAAGTTTTCAGGGTATAGACATGGAACCAACTGCC 166
Qy 61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleYsGluHisIleGlu 80
Db 165 CACGGGAGGCTGTGGATTAACCTATCCAAACTTGTCTTAATTAAGAACACATAGAG 106
Qy 81 ArgGlnLysLysArgCybAlaGlyGluArgTrpArgValThrLysPheLeuAspTrpLeu 100
Db 105 GCCCAAAAAAAGGTGTGCAGAGAAAGATGAGAGTGAACAAGTTCTTACTACTG 46
Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
Db 45 CAAGTATTCTTGGTGTATTAACCGAGTGGACACCGGAAAGT 1

RESULT 15
US-10-787-382-7
; Sequence 7, Application US/10787382
; Publication No. US20040191868A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/10/787,382
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-787-382-7

Alignment Scores:
Pred. No.: 5,99e-78 Length: 402
Score: 610.00 Matches: 115
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0
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US-10-787-382-10 (1-115) x US-10-787-382-7 (1-402)

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QY      1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20
Db      58 TTTCGTGAGAAATCCCATGATATAGACTGGGAGAGACCTTGACACTGCTCCACT 117
QY      21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
Db      118 CATGAACTTGCTGATAGCGGATGGGAACTGATGATTCCTACTCCTGAAAAATAAAT 177
QY      41 HisGlnLeuCysIleLysGluValPheGlnGlyTlleAspThrLeuLysAsnGlnThrAla 60
Db      178 CACCACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 237
QY      61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
Db      238 CACGGGGAGGCTGTGATAACTATCCAAACTTGTCTTAAATAAAGAACACATAGAG 297
QY      81 ArgGlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100
Db      298 CGCCAAAAAAGAGTGTGCAGAGAAAGATGAGAGTGAACAAGTTCTTAGACTACTCTG 357
QY      101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
Db      358 CAAGTATTTCTTGGTGAATAAACACCGAGTGACACCGGAAAGT 402
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Search completed: August 7, 2005, 03:16:01  
Job time : 479.55 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus2n model

Run on: August 6, 2005, 19:45:30 ; Search time 2415 Seconds  
(without alignments)  
1812.584 Million cell updates/sec

Title: US-10-787-382-10  
Perfect score: 610  
Sequence: 1 PAVNPMNRVLAETLTLST.....FLDYLQVFLGVINTEWTPES 115

Scoring table:  
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Xgapop 10.0, Ygapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/cgn2.1/USPPO.spool.p/US10787382/runat.04082005.084752.19305/app.query.fasta.1.590  
-DB=EST -QFMT=fastlap -SUFFIX=rest -MINMATCH=0.1 -LOOFCI=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTMT=ptco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO MMAP -LARGESQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=150 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_hcc:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est1:  
9: gb\_gse2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	356.5	58.4	622	9	CE331159 tigr-gse-
2	356	58.4	405	9	AY412020 Homo sapi
3	356	58.4	456	6	CD559532 AGENCOURT
4	356	58.4	456	6	CD559532 AGENCOURT
5	356	58.4	470	6	CD559532 AGENCOURT
6	356	58.4	492	6	CD559533 AGENCOURT
7	343	56.2	458	3	BC066279 Homo sapi
8	343	56.2	458	3	BC066280 Homo sapi
9	343	56.2	463	6	CD559535 AGENCOURT

c 10	343	56.2	467	6	CD559690	CD559690 AGENCOURT
c 11	343	56.2	473	6	CD559689	CD559689 AGENCOURT
c 12	343	56.2	489	6	CD559536	CD559536 AGENCOURT
c 13	343	56.2	817	3	BC069137	BC069137 Homo sapi
c 14	337	55.2	405	9	AY412021	AY412021 Pan trogl
c 15	332	54.4	456	3	BC066281	BC066281 Homo sapi
c 16	332	54.4	467	6	CD559688	CD559688 AGENCOURT
c 17	332	54.4	478	6	CD559534	CD559534 AGENCOURT
c 18	324	53.1	477	6	CD559608	CD559608 AGENCOURT
c 19	307	50.3	399	9	AY412022	AY412022 Mus muscu
c 20	186	30.5	781	9	CR235404	CR235404 Reverse s
c 21	165	27.0	503	5	BO598873	BO598873 MI-P-B4-a
c 22	91.5	15.0	811	4	BI247887	BI247887 602959820
c 23	86	14.1	412	5	BM573727	BM573727 BM573727
c 24	82.5	13.5	496	1	AA689677	AA689677 v803c02.r
c 25	81	13.3	1267	3	CR727373	CR727373 Tetradon
c 26	80.5	13.2	518	4	BM284184	BM284184 k131b02.y
c 27	80.5	13.2	589	6	CD305286	CD305286 StRp691
c 28	79.5	13.0	618	2	BE920538	BE920538 EST424307
c 29	79.5	13.0	675	4	BT561257	BT561257 603256408
c 30	79	13.0	425	2	AM068198	AM068198 cn23c07.y
c 31	79	13.0	504	6	CB047608	CB047608 NISC_9903
c 32	79	13.0	606	7	CO896018	CO896018 Boven_24
c 33	79	13.0	607	5	BO018244	BO018244 UI-H-DH1-
c 34	79	13.0	644	6	CB047607	CB047607 NISC 9903
c 35	79	13.0	660	7	CN371286	CN371286 170006000
c 36	79	13.0	666	6	CA311187	CA311187 UI-CF-PNO
c 37	79	13.0	721	7	CN480217	CN480217 UI-H-BUO-
c 38	79	13.0	728	6	CA314164	CA314164 UI-CF-PNO
c 39	79	13.0	728	7	CN371285	CN371285 170004245
c 40	79	13.0	736	5	BU619568	BU619568 UI-H-FH1-
c 41	79	13.0	756	4	BG389597	BG389597 602414324
c 42	79	13.0	759	8	BZ542697	BZ542697 OGAROC6TC
c 43	79	13.0	781	5	BU933793	BU933793 AGENCOURT
c 44	79	13.0	812	5	BU631441	BU631441 UI-H-PL0-
c 45	79	13.0	904	4	BM462936	BM462936 AGENCOURT

ALIGNMENTS

RESULT 1  
CE331159  
LOCUS  
DEFINITION tigr-gse-dog-1700033986568 Dog Library Canis familiaris genomic,  
genomic survey sequence.  
ACCESSION CE331159  
VERSION CE331159.1 GI:36147469  
KEYWORDS GSS.  
SOURCE  
ORGANISM Canis familiaris (dog)  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 622)  
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
JOURNAL MEDLINE  
PUBMED 14512627  
COMMENT  
Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: shotgun.  
FEATURES  
source  
1..622  
Location/Qualifiers  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"

ORIGIN

/db\_xref="taxon:9615"  
/clone\_1fb="Dog Library"  
/note="Site 1: Bactxi; Libraries were prepared from  
peripheral blood"

## Alignment Scores:

Pred. No.: 2,32e-35 Length: 622  
Score: 356.50 Matches: 75  
Percent Similarity: 65.22% Conservative: 0  
Best Local Similarity: 65.22% Mismatches: 0  
Query Match: 58.44% Indels: 40  
DB: 9 Gaps: 1

US-10-787-382-10 (1-115) x CB331159 (1-622)

Qy 41 HisglnleuCyglllelygluValPheglnlylleapThrleuysaenglnThrala 60  
Db 42 CACCAACTGTCATTAAAGAGTTTTCAGGATATAGACATTGAAGAACCAACTGCC 101  
Qy 61 HisgylgluAlaValAspLysleuPheglnsaenleuSerleuileysglnHisilegln 80  
Db 102 CACGGAGAGCTGTGATTAACCTATTCCTTTAATTAAGAACACTAGAG 161  
Qy 81 Arggln-Lys----- 83  
Db 162 CGCCAAAAGTAAAGTAAAGACATTGGCAAAACCTTAAGTATATTGTCTGACTGCC 221  
Qy 83 ----- 83  
Db 222 TGTATTTTTTTTTTTTACAAAGATGACAGTTCTCAATATCTCTGTTCTT 281  
Qy 84 -----LysArgCysalaglygluArgTPrArgValThrLysPheleuAspLysleu 101  
Db 282 TTAACAGAAAAGCTGTGAGAGAAAGTGAAGATGACAAAGTTCTTACACTGCA 341  
Qy 101 nvalPheleuGlyValileanThrgluTPrThProgluser 115  
Db 342 AGTATTTCTGTGTATTAACACCGAGTGACACCGAAAGT 384

RESULT 2  
AY412020 405 bp DNA linear GSS 16-DEC-2003  
LOCUS Homo sapiens IL5 gene, VIRUAL TRANSCRIPT, partial sequence,  
GENOMIC SURVEY SEQUENCE.  
ACCESSION AY412020  
VERSION AY412020.1 GI:39767985  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 405)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejelaval,A.,  
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 405)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejelaval,A.,  
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
SOURCE 1. 405  
Location/Qualifiers

ORIGIN

/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
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/gene="IL5"  
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## Alignment Scores:

Pred. No.: 1.5e-35 Length: 405  
Score: 356.00 Matches: 70  
Percent Similarity: 76.79% Conservative: 16  
Best Local Similarity: 62.50% Mismatches: 26  
Query Match: 58.36% Indels: 0  
DB: 9 Gaps: 0

US-10-787-382-10 (1-115) x AY412020 (1-405)

Qy 4 GluAsnProMetAsnArgleuValAlagluThrleuThreuleuSerThrHisArgThr 23  
Db 67 GAAATTCACCAAGATGATGTTGTAAGAGACCTTGACACTGCTTCTACATCGAACT 126  
Qy 24 TPrleuilegylaspglyAsnleuMetileProThrProglusernlysaenHisglnleu 43  
Db 127 CTGCTATAGCCCAATGAGACTCTGAGATTCTGTCTTCTTACATAAAATCAACCACTG 186  
Qy 44 CysileysglnValPheglnlylleapThrleuysaenglnThralaHisilegln 63  
Db 187 TGCACAGAAATCTTTCAGGAAATAGGCACTGAGAGTCAAACTGTGCAAGGGGT 246  
Qy 64 AlaValAspLysleuPheglnsaenleuSerleuileysglnHisilegln 83  
Db 247 ACTGTGAAAGACTATTCAAAACCTTCTTATTAAGAAATCATTTGACGGCAAAA 306  
Qy 84 LysArgCysalaglygluArgTPrArgValThrLysPheleuAspLysleu 103  
Db 307 AAAAAGTGTGAGAAAGAACCGAGAGTAAACCAATTTCTTACACTGCAAGAGTTT 366  
Qy 104 leuGlyValileanThrgluTPrThProgluser 115  
Db 367 CTGCTATTAAGAACCGAGTGTGATTAAGAAAGT 402

RESULT 3  
CD559532 456 bp mRNA linear EST 11-JUN-2003  
LOCUS CD559532  
DEFINITION AGENCOURT 14497057 NIH\_MGC\_195 Homo sapiens CDNA clone  
IMAGE:6971772 5', mRNA sequence.  
ACCESSION CD559532  
VERSION CD559532.1 GI:31585600  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 456)  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics / NIH  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgdbs-remail.nih.gov  
Tissue Procurement: Narayan Bhat  
CDNA Library Preparation: Bhat Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.jnl.gov  
plate: IRB1 row: 9 column: 11  
High quality sequence stop: 456.  
Location/Qualifiers

## SOURCE

1. .456  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/tissue\_type="mixed"  
/lab\_host="DH5A (T1 phage-resistant)"  
/clone\_lib="NIH MGC 195"  
/note="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2:  
loxp-HindIII; Clones from this library have been  
PCR-amplified using gene-specific primers to contain the  
complete open reading frame (based on known gene sequences  
available from NCBI's RefSeq). Template for PCR is cDNA  
derived from either pooled cytoplasmic polyA RNA from 30  
cells lines or pooled total RNA from 10 different tissues  
(from BD Biosciences/Clontech and Washington University).  
PCR products are directionally cloned into the loxp sites  
of the pDNR-Dual vector. Library constructed by Dr.  
Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
Expression Laboratory, Research Technology Program, SAIC  
Frederick, NCI-Frederick, Frederick, MD 21702). For  
information on which gene each clone represents, please  
visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearrayed\_plates/IRBK.presv.dat  
a Note: this is a NIH\_MGC library."

## ORIGIN

## Alignment Scores:

Pred. No.: 1.76e-35 Length: 456  
Score: 356.00 Matches: 70  
Percent Similarity: 76.79% Conservative: 16  
Best Local Similarity: 62.50% Mismatches: 26  
Query Match: 58.36% Indels: 0  
DB: Gaps: 0

US-10-787-382-10 (1-115) x CD559532 (1-456)

OY 4 GUAENPROMETAANAGLEUVALAAGLUHRLIEUTHRLIEUSERTHNIAARGTHR 23  
DB 88 GAAATTTCCACAGAAATGCTTGTAAGAGACCTTGCGACTTCTTACTCATCGAACT 147  
OY 24 TRLPULIEGLYASRPGLYASNLEUMETLEPROTHRPROGLUASNLVASNHIEGLNLEU 43  
DB 148 CTGCTGATAGCCAAATGAGACTCTGAGATCTCTGCTTCTGATACATTAATACCAACTG 207  
OY 44 CYSILLEYGULVALPHEGLINGLYLEASRTHRLIEUVAENGLNTHRALHIEGLYGLU 63  
DB 208 TGCACTGAAGAAATCTTCAAGGAATAGGACACTGAGAGACGCAAACTGTCAGAGGGGT 267  
OY 64 ALAVALAPRYLVEUPHIEGLINLEUSETLEULIEYSGLUHIEGLIEGLUARGGLNLYS 83  
DB 268 ACTGTGGAAGAAGCTTAATCAAAACCTTGCTTAATAAGAAATACATTGACGGCCAAA 327  
OY 84 LYSARGCYBALAGLYGLUARGTRPARGVATHRYSRPHLEUAPRYTLEUGLINVALPHE 103  
DB 328 AAAAAGTGTGAGAAAGAAAGACGAGTAACCAATTCCTTACCTTACCTGCAAGAGTTT 387  
OY 104 LEUGLYVALILEASRTHRLIEUPTHRPROGLUSER 115  
DB 388 CTTGGTGTATGAAACACCGAGTGAATTAATGAAGAACT 423

## RESULT 4

CD559686/c

LOCUS CD559686 456 bp mRNA linear EST 11-JUN-2003  
DEFINITION AGENCOURT 14497093 NIH MGC 195 Homo sapiens cDNA clone  
IMAGE:6971772 3', mRNA sequence.

ACCESSION

CD559686  
VERSION CD559686.1 GI:31585754

KEYWORDS

EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 456)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: gcgabs-remail.nih.gov

Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: Bhat Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: IRBK1 row: 9 column: 11  
High quality sequence stop: 456.  
Location/Qualifiers

## FEATURES

## SOURCE

1. .456  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:6971772"  
/tissue\_type="mixed"  
/lab\_host="DH5A (T1 phage-resistant)"  
/clone\_lib="NIH MGC 195"  
/note="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2:  
loxp-HindIII; Clones from this library have been  
PCR-amplified using gene-specific primers to contain the  
complete open reading frame (based on known gene sequences  
available from NCBI's RefSeq). Template for PCR is cDNA  
derived from either pooled cytoplasmic polyA RNA from 30  
cells lines or pooled total RNA from 10 different tissues  
(from BD Biosciences/Clontech and Washington University).  
PCR products are directionally cloned into the loxp sites  
of the pDNR-Dual vector. Library constructed by Dr.  
Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
Expression Laboratory, Research Technology Program, SAIC  
Frederick, NCI-Frederick, Frederick, MD 21702). For  
information on which gene each clone represents, please  
visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearrayed\_plates/IRBK.presv.dat  
a Note: this is a NIH\_MGC library."

## ORIGIN

## Alignment Scores:

Pred. No.: 1.76e-35 Length: 456  
Score: 356.00 Matches: 70  
Percent Similarity: 76.79% Conservative: 16  
Best Local Similarity: 62.50% Mismatches: 26  
Query Match: 58.36% Indels: 0  
DB: Gaps: 0

US-10-787-382-10 (1-115) x CD559686 (1-456)

OY 4 GUAENPROMETAANAGLEUVALAAGLUHRLIEUTHRLIEUSERTHNIAARGTHR 23  
DB 367 GAAATTTCCACAGAAATGCTTGTAAGAGACCTTGCGACTTCTTACTCATCGAACT 308  
OY 24 TRLPULIEGLYASRPGLYASNLEUMETLEPROTHRPROGLUASNLVASNHIEGLNLEU 43  
DB 307 CTGCTGATAGCCAAATGAGACTCTGAGATCTCTGCTTCTGATACATTAATACCAACTG 248  
OY 44 CYSILLEYGULVALPHEGLINGLYLEASRTHRLIEUVAENGLNTHRALHIEGLYGLU 63  
DB 247 TGCACTGAAGAAATCTTCAAGGAATAGGACACTGAGAGTCAAACTGTCAGAGGGGT 188  
OY 64 ALAVALAPRYLVEUPHIEGLINLEUSETLEULIEYSGLUHIEGLIEGLUARGGLNLYS 83  
DB 187 ACTGTGGAAGAAGCTTAATCAAAACCTTGCTTAATAAGAAATACATTGACGGCCAAA 128  
OY 84 LYSARGCYBALAGLYGLUARGTRPARGVATHRYSRPHLEUAPRYTLEUGLINVALPHE 103

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Db      127  AAAAGGTGGAGAGAAACGAGGAGTAACCAATCTCAGCTCAAGAGTTT 68
Qy      104  LeuGlyValIleAenThrGluTrpThrProGluSer 115
Db      67  CTGGTGTAAATGAACCGAGTGATATATAGAAAGT 32

RESULT 5
CD559687/c 470 bp  mRNA  linear  EST 19-NOV-2003
LOCUS      AGENCOURT_14497029 NIH_MGC_195 Homo sapiens cDNA clone
DEFINITION IMAGE:6971771 5', mRNA sequence.
ACCESSION  CD559687
VERSION     CD559687.2 GI:38453484
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1  (bases 1 to 470)
AUTHORS    NIH-MGC http://mgs.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585755.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cga@nci.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: IRBKL row: 9 column: 10
            High quality sequence start: 14
            High quality sequence stop: 470.
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                        /clone_lib="NIH_MGC_195"
                        /note="Vector: pDNR-Dual; Site_1: loxp-sali; Site_2:
                        loxp-HindIII; Clones from this library have been
                        PCR-amplified using gene-specific primers to contain the
                        complete open reading frame (based on known gene sequences
                        available from NCBI's RefSeq). Template for PCR is cDNA
                        derived from either pooled cytoplasmic polyA RNA from 30
                        cells lines or pooled total RNA from 10 different tissues
                        (from BD Biosciences/Clontech and Washington University).
                        PCR products are directionally cloned into the loxp sites
                        of the pDNR-dual vector. Library constructed by Dr.
                        Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                        Expression Laboratory, Research Technology Program, SAIC
                        Frederick, NCI-Frederick, Frederick, MD 21702). For
                        information on which gene each clone represents, please
                        visit our anonymous ftp site at
                        ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
                        a Note: this is a NIH_MGC Library."

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DB:      6      Gaps:      0
US-10-787-382-10 (1-115) x CD559687 (1-470)
Qy      4  GluAsnProMetLeuAlaGluThrIleuThrIleuSerThrIleArgThr 23
Db      380  GAATATCCCAAGATGATGATGAAAGACCTTGACACTGCTTACTACATGAACT 321
Qy      24  TrpLeuIleGlyAsnProGluMetIleProThrProGluAsnIleGlyLeu 43
Db      320  CTGCTGATAGCCAAATGAGACTCTGAGATTCCTCTCTGACTTAAATACCAACTG 261
Qy      44  CysIleGlyLeuAlaPheGluIleAspThrIleuLeuAsnGlnThrAlaIleGlyGlu 63
Db      260  TGCACTGAAGAATCTTTCAGGGAATGACCACTGAGATCAAACTGTGCAAGGGGT 201
Qy      64  AlaValAspLeuPheGlnAsnIleuSerIleuIleGlyGluIleGlyArgGlnIle 83
Db      200  ACTGTGAAGAACTATTCAAAACTTCTCTTAAAGAAATCATTTGACGGCCAAA 141
Qy      84  LysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGlnValPhe 103
Db      140  AAAAAGTGTGAGAAAGAAACGAGAGTAACCAATCTCAGCTCAAGAGTTT 81
Qy      104  LeuGlyValIleAenThrGluTrpThrProGluSer 115
Db      80  CTGGTGTAAATGAACCGAGTGATATATAGAAAGT 45

RESULT 6
CD559533 492 bp  mRNA  linear  EST 26-NOV-2003
LOCUS      AGENCOURT_14496993 NIH_MGC_195 Homo sapiens cDNA clone
DEFINITION IMAGE:6971771 5', mRNA sequence.
ACCESSION  CD559533
VERSION     CD559533.2 GI:38558947
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1  (bases 1 to 492)
AUTHORS    NIH-MGC http://mgs.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585601.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cga@nci.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: IRBKL row: 9 column: 10
            High quality sequence start: 14
            High quality sequence stop: 492.
            Location/Qualifiers
                source
                    1..492
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
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                        /clone="IMAGE:6971771"
                        /tissue_type="mixed"
                        /lab_host="DH5A (TI phage-resistant)"
                        /clone_lib="NIH_MGC_195"
                        /note="Vector: pDNR-Dual; Site_1: loxp-sali; Site_2:
                        loxp-HindIII; Clones from this library have been
                        PCR-amplified using gene-specific primers to contain the
                        complete open reading frame (based on known gene sequences

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ORIGIN
Alignment Scores:
Pred. No.:      1,84e-35      Length:      470
Score:          356.00      Matches:      70
Percent Similarity: 76.7%      Conservative: 16
Best Local Similarity: 62.50%      Mismatches: 26
Query Match:    58.36%      Indels:      0

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available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the Ixp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongliang Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [ftp://image.llnl.gov/image/rearray\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearray_plates/IRBK.presv.dat) a Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.96e-35 Length: 492  
 Score: 356.00 Matches: 70  
 Percent Similarity: 76.79% Conservative: 16  
 Best Local Similarity: 62.50% Mismatches: 26  
 Query Match: 58.36% Indels: 0  
 DB: 6 Gaps: 0

US-10-787-382-10 (1-115) x CD559533 (1-492)

Qy 4 GluAnpPromeAaAaAgluValAlaGluThrLeuThrLeuSerThrHisArgThr 23  
 Db 122 GAATTTCCCAACAGATGATGTAAGAGACCTTGACACCTGCTTCTACATCGAACT 181  
 Qy 24 TrrleuilegluAerGluAenleuMetileProThrProGluAenluAenHieGluLeu 43  
 Db 182 CTGCTGATAGCCATGAGACTCTGAGACTCTCTCTCTGACATTAATAATCACAACATG 241  
 Qy 44 CyeileysgluValPheGlnGlyLeaPrrThrleuAenGlnThralHieGlyGlu 63  
 Db 242 TGCACTGAAGAACTTTCAAGGAAATGAGCACACTGAGAGACTCAAACTGTCAAGGGGGT 301  
 Qy 64 AlavaAlaplysleupheGlnAenleuSerleuileysgluHieGluAryGlnlys 83  
 Db 302 ACTGTGAAAGACATTAATAAACTGCTTAATAAAAGAAATACATTTAGCGCCAAA 361  
 Qy 84 LysArgCysAlaGluArgTrpArgValThrIysPheleuAerGlyLeuGlnValPhe 103  
 Db 362 AAAAAGTGTGAGAAAGAAAGCGAGAGTAACAATCCATGACTACCTGCAAGAGTTT 421  
 Qy 104 LeuGlyValIleAenThrGluTrpThrProGluSer 115  
 Db 422 CTGTGTATATGAACACCGAGTGAATATAGAAAGT 457

## RESULT 7

BC066279 458 bp mRNA linear HTC 12-FEB-2004  
 LOCUS Homo sapiens cDNA clone IMAGE:6971768, containing frame-shift errors.  
 ACCESSION BC066279  
 VERSION BC066279.1 GI:42490901  
 KEYWORDS HTC.  
 ORGANISM Homo sapiens (human)  
 SOURCE Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 458)  
 Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stedelson,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Udutin,T.B., Toshitsuki,S., Carman,C., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McEwan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulys,S.W.,

TITLE  
 JOURNAL  
 PUBMED  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL

REMARK  
 COMMENT

Villalon,D.K., Muzny,D.M., Sodergren,B.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,J., Whiting,M., Madan,A., Young,A.C., Rodriguez,S., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,B.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Scherzer,A., Schein,J.B., Jones,S.J. and Marr,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 2 (bases 1 to 458)  
 Strausberg,R.  
 Direct Submission  
 Submitted (03-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: Narayan Bhat  
 cDNA Library Preparation: Bhat Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMNI)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web Site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILMNI at: <http://image.llnl.gov>  
 Series: IRBK Plate: 172 Row: a Column: 15  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28559032  
 This clone has the following problem: frame shifted.

## FEATURES

## SOURCE

location/qualifiers  
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## ORIGIN

Alignment Scores:  
 Pred. No.: 8.5e-34 Length: 458  
 Score: 343.00 Matches: 70  
 Percent Similarity: 76.11% Conservative: 16  
 Best Local Similarity: 61.95% Mismatches: 26  
 Query Match: 56.23% Indels: 1  
 DB: 3 Gaps: 0

US-10-787-382-10 (1-115) x BC066279 (1-458)

Qy 4 GluAnpPromeAaAaAgluValAlaGluThrLeuThrLeuSerThrHisArgThr 23  
 Db 90 GAATTTCCCAACAGATGATGTAAGAGACCTTGACACCTGCTTCTACATCGAACT 149  
 Qy 24 TrrleuilegluAerGluAenleuMetileProThrProGluAenluAenHieGluLeu 43  
 Db 150 CTGCTGATAGCCATGAGACTCTGAGACTCTCTCTCTGACATTAATAATCACAACATG 209  
 Qy 44 CyeileysgluValPheGlnGlyLeaPrrThrleuAenGlnThralHieGlyGlu 63  
 Db 210 TGCACTGAAGAACTTTCAAGGAAATGAGCACACTGAGAGACTCAAACTGTCAAGGGGGT 269  
 Qy 64 AlavaAlaplysleupheGlnAenleuSerleuileysgluHieGluAryGln-ly 83

Db 270 ACTGTGGAAGACTATTCAAAAACCTTGCTCTTAATAAGAAATACATTGACGGCCAAAA 329  
Qy 83 slyvargCyAalGlyGluArgValThrLyPheLeuAspTyrLeuGlnValPh 103  
Db 330 AAAAAATGTGGAGAAAGAAAGACGAGAGTAACCAATTCTTACTGACCTGCAAGATT 389  
Qy 103 eleuGlyValIleAsnThrGluTyrThrProGluSer 115  
Db 390 TCTTGTGTATGATGAAACCGATGATATATGAAAGT 426

RESULT 8  
BC066280 458 bp mRNA linear HTC 12-FEB-2004  
LOCUS Homo sapiens cDNA clone IMAGE:6971769, containing frame-shift errors.  
ACCESSION BC066280  
VERSION BC066280.1 GI:42490838  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 458)  
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Scheffer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Datchenko,L., Marusik,K., Farmer,A., Rubin,G.M., Hong,L., Staptieno,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Uddin,T.B., Tomihata,S., Carninci,P., Frange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McGowan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hultk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Sanchez,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalins,D.E., Scherch,A., Schein,J.B., Jones,S.J. and Marra,M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 458)  
AUTHORS Strausberg,R.  
DIRECT SUBMISSION  
SUBMITTED (03-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
CONTACT: MGC help desk  
EMAIL: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: Bhat Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
CONTACT: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Series: IRAX Plate: 172 Row: a Column: 16  
This clone was selected for full length sequencing because it passed the following selection criteria: matched RNA gi: 28559032  
This clone has the following problem: frame shifted.  
FEATURES  
SOURCE Location/Qualifiers  
1..458

/organism="Homo sapiens"  
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/clone\_id="NIH\_MGC\_195"  
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ORIGIN

Alignment Scores:

Pred. No.:	8,5e-34	Length:	458
Score:	343.00	Matches:	70
Percent Similarity:	76.11%	Conservative:	16
Best Local Similarity:	61.95%	Mismatches:	26
Query Match:	56.23%	Indels:	1
DB:	3	Gaps:	0

US-10-787-382-10 (1-115) x BC066280 (1-458)

Qy 4 GluAspProMetLeuValAlaGluThrLeuThrLeuLeuSerThrHisArgThr 23  
Db 90 GAAATCCCAAGACTGATTCGTAAGAGACCTTGCACTGCTTCTACTCATCGAAT 149  
Qy 24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnIleGlnLeu 43  
Db 150 CTGCTGTATCCATGATGACTGAGGATTCCTGTTCTGTATATAAAATCCAACTG 209  
Qy 44 CysIleLeuGluValPheGlnGlyIleAspThrLeuLeuAsnGlnThrAlaHleGlyGlu 63  
Db 210 TGCACCTGAAATAATCTTCAGGAAATGCGACCTGAGAGTCMAACTGTCGCAAGGGGT 269  
Qy 64 AlaValAspLeuPheGlnAsnLeuSerLeuIleLeuGluHisIleGluArgGln-Ly 83  
Db 270 ACTGTGGAAGACTATTCAAAAACCTTGCTCTTAATAAGAAATACATTGACGGCCAAAA 329  
Qy 83 slyvargCyAalGlyGluArgValThrLyPheLeuAspTyrLeuGlnValPh 103  
Db 330 AAAAAATGTGGAGAAAGAAAGACGAGAGTAACCAATTCTTACTGACCTGCAAGATT 389  
Qy 103 eleuGlyValIleAsnThrGluTyrThrProGluSer 115  
Db 390 TCTTGTGTATGATGAAACCGATGATATATGAAAGT 426

RESULT 9  
CD559535 463 bp mRNA linear EST 26-NOV-2003  
LOCUS AGENCOURT\_14496865 NIH\_MGC\_195 Homo sapiens cDNA clone  
DEFINITION IMAGE:6971769 5', mRNA sequence.  
ACCESSION CD559535  
VERSION CD559535.2 GI:38558950  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 463)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLES Unpublished (1999)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585603.  
CONTACT: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
EMAIL: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: Bhat Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Plate: IRBK1 row: 9 column: 08  
High quality sequence stop: 463.

## FEATURES

## Source

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/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH MGC 195"
/notes="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Barayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat"
Note: this is a NIH MGC library."

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**ORIGIN**

### Alignment Scores:

Pred. No.:	8.63e-34	Length:	463
Score:	343.00	Matches:	70
Percent Similarity:	76.11%	Conservative:	16
Best Local Similarity:	61.95%	Mismatches:	26
Query Match:	56.23%	Indels:	1
DB:	6	Gaps:	0

US-10-787-382-10 (1-115) x CD559535 (1-463)

Qy	4	GLuAsnProMetAsnAspArgLeuValAlaGluThrLeuThrLeuLeuSerThrHisAspThr	23
Db	94	GAATTCCTCCACAAAGTCATGTGGTGAAGAAGACCTTGCGACTGCTTCTACTCATCGAACT	153
Qy	24	TrpLeuIleGlyAspGlyAsnLeuNecIleProThrProGluAsnIlyAsnHisGlnLeu	43
Db	154	CTGCGAATGAGCCAAAGACACTGTGAGGATTCCTGTCTCTGTACATAAAATACCCAACTG	213
Qy	44	CysIleIysGluValPheGlnGlyIleAspThrLeuIysAsnGlnThrHisIleGlyGlu	63
Db	214	TGCATGTGAAGAAATCTTTTCAGGGAATAGGCACACTGAGACGTCAAACTGTGCAGGGGCT	273
Qy	64	AlaValAspIlyLeuPheGlnIleAsnLeuSerLeuIleGlyGluHisIleGluArgGln-Ly	83
Db	274	ACTGTGGAAGACTAATTCAAAACTGTCTTAATTAAGAAATATCACTTGACGGCCAAAAA	333
Qy	83	SlyAspArgCysAlaGlyGluArgTrpArgValThrIlyPheLeuAspTyrLeuGlnValPrl	103
Db	334	AAAAAAGCTGGAAGAAAGAACGAGAACTAAACCAATTCCTAGACTCACTGCAGAGTT	393
Qy	103	eleuGlyValIleAsnThrGluThrProGluSer	115
Db	394	TCTTGTTGTAAATGAACACCGATGTGATATAGAAACT	430

RESULT	10				
CD559690/c					
LOCUS		467 bp	mRNA	linear	EST 19-NOV-2003
DEFINITION	CD559690				
	AGENCOURT 14496838 NIH_MGC_195 Homo sapiens				
	IMAGE:6971768 5', mRNA sequence.				
ACCESSION	CD559680				
VERSION	CD559690.2				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				

## ORGANISM

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 467)
TITLE	NH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished. (1999) On Jun 10, 2003 this sequence version replaced gi:31585758.

## FEATURES

## Source

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1. 467
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    /mol_type="mrna"
    /db_xref="taxon:9606"
    /clone="IMAGE:6971768"
    /tissue_type="mixed"
    /lab_host="DH5A (/11 phage-resistant)"
    /clone_1fb="NIH MGC 195"

    /note="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2:
    /loxP-HindIII; Clones from this library have been
    PCR-amplified using gene-specific primers to contain the
    complete open reading frame (based on known gene sequences
    available from NCBI's RefSeq). Template for PCR is cDNA
    derived from either pooled cytoplasmic polyA RNA from 30
    cells lines or pooled total RNA from 10 different tissues
    (from BD Biosciences/Clontech and Washington University).
    PCR products are directionally cloned into the loxp sites
    of the pDNR-Dual vector. Library constructed by Dr.
    Narayan Bhat, Earl Bete III and Hongling Liao (Gene
    Expression Laboratory, Research Technology Program, SAIC
    Frederick, NCI-Frederick, Frederick, MD 21702). For
    information on which gene each clone represents, please
    visit our anonymous ftp site at
    ftp://image.lln.gov/image/rearranged/plates/IRBX.presv.dat"
    A Note: this is a NIH MGC Library. "

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**ORIGIN**

### Alignment Scores:

Pred. No.:	8,73e-34	Length:	467
Score:	343.00	Matches:	70
Percent Similarity:	76.1%	Conservative:	16
Best Local Similarity:	61.95%	Mismatches:	26
Query Match:	56.23%	Indels:	1
DB:	6	Gaps:	0

US-10-787-382-10 (1-115) x CD559690 (1-467)

[illegible]



/note="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [ftp://image.llnl.gov/image/rearrayed\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat) A Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 9,29e-34 Length: 489  
 Score: 343.00 Matches: 70  
 Percent Similarity: 76.11% Conservatave: 16  
 Best Local Similarity: 61.95% Mismatches: 26  
 Query Match: 56.23% Indels: 1  
 DB: Gaps: 0

US-10-787-382-10 (1-115) x CD559536 (1-489)

Qy 4 GluAnpPromeAaArgLeuValAlaGluThrLeuThrLeuLeuSerThriSaArgThr 23  
 Db 120 GAAATTCACAGAGCATTTGGTGAAGAGCATTTGGACATGCTTTCATCATCACTGA 179  
 Qy 24 TrrleuilegIyAspGlyAsnLeuMetIleProThrProGluAnpLysAsnHisGlnLeu 43  
 Db 180 CTGCTGATAGCCAAATGAGACTCTGAGATTCCTGTTCTGTACATATAAAATCACCAC 239  
 Qy 44 CysIlelysgIuValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHisGlyGlu 63  
 Db 240 TGCACTGAAGAAATCTTCAGGAAATGAGCACTGAGAGTCAAACTGTGCAGAGGCT 299  
 Qy 64 AlAlaValAspLysPheGlnAsnLeuSerLeuIleLysGluHisIleGluArgGln-Ly 83  
 Db 300 ACTGTGAAAGACTTTCAAAACCTTGTCTTAAAGAAATACATTGACGCCAAATA 359  
 Qy 83 sIyAsArgCysAlaGlyIuArgTTPArgValThrLysPheLeuAspTyrLeuGlnValPh 103  
 Db 360 AAAAAAGTGGAGAAAGAACGAGATTAACCAATTCCTAGACTACCTGCAAGAGT 419  
 Qy 103 eleuGlyValIleAsnThrGluTrrThrProGluSer 115  
 Db 420 TCTTGTTGTAATGACACCGAGTGTATATAGAAAGT 456

RESULT 13  
 BC069137 817 bp mRNA linear HTC 26-APR-2004  
 DEFINITION Homo sapiens cDNA clone IMAGE:7216996, containing frame-shift error.

ACCESSION BC069137  
 VERSION BC069137.1 GI:46575644  
 KEYWORDS HTC  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 817)  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Klausner,R.D., Collins,F.S., Wagner,L.H., Derge,J.G., Altschul,S.F., Zeeberg,B., Bueow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Ditchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schaefer,T.E., Brownstein,M.J., Uedlin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loguelfano,N.A., Peters,G.J., Abramson,R.D., Muliahy,S.J., Bosak,S.A., McGowan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.D., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,I.S., Krzywicki,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.B., Jones,S.J., and Marra,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 1247932  
 2 (bases 1 to 817)  
 Strauberg,R.  
 Direct Submission  
 Submitted (16-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: Anup Madan, University of Iowa  
 cDNA Library Preparation: Anup Madan, University of Iowa  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Neurogenomics Research Lab,  
 200 B EMBR, University of Iowa, Iowa City, IA-52242  
 anup-madan@uiowa.edu  
 Jessica Fahey, Tim Nelson, Jae Geon Yoon and Anup Madan

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: Plates: Row: Column: 0  
 This clone has the following problem: frame shifted.

## FEATURES

location/qualifiers  
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## ORIGIN

Alignment Scores:  
 Pred. No.: 1.87e-33 Length: 817  
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 Percent Similarity: 76.11% Conservatave: 16  
 Best Local Similarity: 61.95% Mismatches: 26  
 Query Match: 56.23% Indels: 1  
 DB: Gaps: 0

US-10-787-382-10 (1-115) x BC069137 (1-817)

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 Db 111 GAAATTCACAGAGCATTTGGTGAAGAGCATTTGGACATGCTTTCATCATCACTGA 170  
 Qy 24 TrrleuilegIyAspGlyAsnLeuMetIleProThrProGluAnpLysAsnHisGlnLeu 43  
 Db 171 CTGCTGATAGCCAAATGAGACTCTGAGATTCCTGTTCTGTACATATAAAATCACCAC 230  
 Qy 44 CysIlelysgIuValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHisGlyGlu 63  
 Db 231 TGCACTGAAGAAATCTTCAGGAAATGAGCACTGAGAGTCAAACTGTGCAGAGGCT 290  
 Qy 64 AlAlaValAspLysPheGlnAsnLeuSerLeuIleLysGluHisIleGluArgGln-Ly 83

Db 291 ACTGTGGAAGACTATTCACAAACTCTCTTATTAAGAAATACATGACGGCCAAA 350  
 Oy 83 slyarGcYcAlaqlYgluarGTpArGValThlyePheleuapryleuGlnValPh 103  
 Db 351 GAAATAATGTGAGAGAAAGAAACGAGAGTAACCAATTCCTAGACTACCTGCAAGATT 410  
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 RESULT 14  
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 genomic survey sequence.  
 ACCESSION AY412021  
 VERSION AY412021.1 GI:39767986  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM  
 Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.  
 REFERENCE 1 (bases 1 to 405)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous  
 gene trices  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 405)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
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 Gaps: 0  
 DB: 9  
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 Db 67 GAATTCGCCACAGATGATGCTGTGAAGAGACCTTGGACATGCTTCTACATCACTGAACT 126  
 Oy 24 TripleuilegilyaapGlyAanleuMetleleProthrProgluaanlyAanHieGlnleu 43  
 Db 127 CTGTATTAATAGCAATGAGACTCTGAGATTCCTCTCTGCTTAATAAAACACCAACNN 186  
 Oy 44 CyslleuysgluValPheGlnGlylleaPthrleuysAanGlnThriAheGlyGlu 63  
 Db 187 NGCACTGAAGAAATCTTCAAGGAATAGCGACACTGAGAGTCAAACTGTGCAGAGGGGT 246

Oy 64 AlValaAspyleuPheGlnAanleuSerleuileysGlnHieGlyuargGlnlys 83  
 Db 247 ACTGTGGAAGACTATTCACAAACTCTCTTATTAAGAAATACATGAGCCAAA 306  
 Oy 84 lyarGcYcAlaqlYgluarGTpArGValThlyePheleuapryleuGlnValPhe 103  
 Db 307 AAAAAGTGTGAGAGAAAGAAACGAGAGTAACCAATTCCTAGACTACCTGCAAGATT 366  
 Oy 104 leuGlyValilleaanthrglutrPrthrProgluSer 115  
 Db 367 CTGTGTATATGAAACACGAGTGATATATGAAAGT 402  
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 LOCUS  
 DEFINITION Homo sapiens cDNA clone IMAGE:6971770, containing frame-shift  
 errors.  
 ACCESSION BC066281  
 VERSION BC066281.1 GI:42490969  
 KEYWORDS HTC.  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 456)  
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
 Klauener,R.D., Collins,F.S., Wagner,J., Shenmen,C.M., Schuler,G.D.,  
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 Clone distribution: MGC clone distribution information can be found  
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 Series: IRAC Plate; 172 Row; a Column; 17  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 28559032  
 This clone has the following problem: frame shifted.



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